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"Examiner Search Notes"

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James Martinell
Primary Examiner 1631

Martinell, J.
09/989919
Seq ID 15 Issued & Pg Pubs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: December 12, 2003, 18:26:31 ; Search time 18.5 Seconds
(without alignments)
6390.083 Million cell updates/sec

Title: US-09-989-919-15
Perfect score: 2527
Sequence: 1 ggtgctgcacctgtaccgga.....aaaaaaaaaaaaaggcggtc 1397

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09989919_@CGN_1_1_27_@runat_12122003_154548_20369 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	132	5.2	743	4	US-09-252-991A-28327	Sequence 28327, A
c	2	126.5	4.9	299	4	US-09-252-991A-17588	Sequence 17588, A
c	3	124	4.8	1239	1	US-08-026-138E-3	Sequence 3, Appli
	4	120	4.7	439	4	US-09-252-991A-20570	Sequence 20570, A
	5	120	4.7	1964	4	US-09-467-997-1	Sequence 1, Appli
c	6	119	4.6	1063	1	US-08-093-453B-3	Sequence 3, Appli
c	7	118	4.6	897	1	US-07-960-389-2	Sequence 2, Appli
c	8	117	4.6	1184	4	US-09-266-225D-18	Sequence 18, Appl
c	9	117	4.6	1185	3	US-09-041-886-23	Sequence 23, Appl
c	10	116	4.5	433	3	US-09-046-158A-2	Sequence 2, Appli
c	11	115	4.5	907	3	US-08-783-774-2	Sequence 2, Appli
c	12	115	4.5	907	4	US-09-328-599A-1	Sequence 1, Appli
c	13	115	4.5	907	5	PCT-US95-04611A-19	Sequence 19, Appl
c	14	115	4.5	1063	1	US-08-127-499A-8	Sequence 8, Appli
c	15	115	4.5	1063	1	US-08-482-847-8	Sequence 8, Appli
	16	114	4.5	593	4	US-09-252-991A-20441	Sequence 20441, A
c	17	113	4.4	472	4	US-09-252-991A-31978	Sequence 31978, A
c	18	112.5	4.4	376	4	US-08-874-569B-20	Sequence 20, Appl
c	19	112.5	4.4	376	4	US-09-955-518-20	Sequence 20, Appl
c	20	112	4.4	697	4	US-09-252-991A-24009	Sequence 24009, A
c	21	112	4.4	992	1	US-08-127-499A-1	Sequence 1, Appli
c	22	112	4.4	992	1	US-08-482-847-1	Sequence 1, Appli
	23	111	4.4	414	4	US-09-252-991A-24714	Sequence 24714, A
	24	110	4.4	520	4	US-09-252-991A-27089	Sequence 27089, A
c	25	109.5	4.3	525	4	US-09-252-991A-23981	Sequence 23981, A
c	26	109.5	4.3	1298	2	US-08-690-473-2	Sequence 2, Appli
c	27	109.5	4.3	1298	3	US-09-259-821A-2	Sequence 2, Appli
c	28	109.5	4.3	1298	3	US-08-843-659-2	Sequence 2, Appli
c	29	109	4.3	1130	4	US-09-442-100-4	Sequence 4, Appli
c	30	109	4.3	1130	4	US-09-233-857-3	Sequence 3, Appli
c	31	109	4.3	1130	4	US-08-939-106-4	Sequence 4, Appli
c	32	108	4.2	442	4	US-09-252-991A-23285	Sequence 23285, A
c	33	107	4.2	330	4	US-09-252-991A-26360	Sequence 26360, A
	34	107	4.2	486	4	US-09-252-991A-20637	Sequence 20637, A
c	35	106.5	4.2	178	4	US-09-252-991A-31386	Sequence 31386, A
	36	106.5	4.2	188	4	US-09-252-991A-28878	Sequence 28878, A
c	37	106.5	4.2	504	4	US-09-252-991A-28242	Sequence 28242, A
c	38	106	4.1	395	4	US-09-252-991A-31694	Sequence 31694, A
c	39	106	4.1	878	4	US-09-556-706B-2	Sequence 2, Appli
c	40	105.5	4.1	323	4	US-09-252-991A-23885	Sequence 23885, A
	41	105	4.2	313	4	US-09-252-991A-27480	Sequence 27480, A
c	42	105	4.1	557	3	US-08-927-219-139	Sequence 139, App
c	43	105	4.1	595	4	US-09-252-991A-18995	Sequence 18995, A
c	44	105	4.1	962	4	US-09-442-100-6	Sequence 6, Appli
c	45	105	4.1	962	4	US-08-939-106-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-28327
; Sequence 28327, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28327
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28327

Alignment Scores:

Pred. No.:	8.86e-05	Length:	743
Score:	132.00	Matches:	114
Percent Similarity:	34.31%	Conservative:	38
Best Local Similarity:	25.73%	Mismatches:	181
Query Match:	5.22%	Indels:	110
DB:	4	Gaps:	21

US-09-989-919-15 (1-1397) x US-09-252-991A-28327 (1-743)

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Db         355 CysLeuAlaProGlyAlaArgAlaArgGlnProAspLeuArgGlyAlaAspArgThrGly 374
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Qy        72 GTATCCCAGACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACG 131
Db       375 AlaGlyAlaValAlaGlyAlaAlaArgArgThrAlaAlaArgGly-------------- 389

Qy       132 GGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATG 191
Db       390 --------------------------------ArgArgProArgSerArgProAlaLeu 398

Qy       192 CCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTG---AGCCAGTGG 248
Db       399 ProGly---GlyPro--------------ArgProAlaGlyGlnProAspAlaArgPro 412

Qy       249 GAGAAGCCCTTC----------------------------CAAGGGAGATGGCAGGAC 278
Db       413 AspArgProAlaProArgAlaProValProAlaAlaGlyProArgGlyArgGlyArgAla 432

Qy       279 CTC---TCTGGAGGTTGATAGATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGG 335
Db       433 LeuValSerAlaGlyAlaGlyAlaGlyThrGlyGluSerArgSerLeuGlyAlaLeuArg 452

Qy       336 TGATGAGAGAGAGGTATACGTGTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCT 395
Db       453 LeuProGlyThrGlyLeuAlaGlyGlyArgAlaGlyArgProGlyArgGlyValGlnPro 472

Qy       396 CCA------------GAAAGAGAAACATCCAGCCCTGTTACCTCTCACCTCTGCCCCCCA 443
Db       473 ProAlaGlyGlyArgThrAlaAspAlaAlaAlaPro--------------CysPro--- 486

Qy       444 GGTCGGCAGCTGGTCTTTTTCAAGACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAG 503
Db       487 ---ArgSerAlaValSerArgArgAlaAlaAlaGlyGlnLeuArgProAspProAlaAla 505

Qy       504 ACCACATATGTGAAGGCCTCTGGCTGACCTATCTGAGGGCTCGGCTGACCAGCTGACTAT 563
Db       506 GlyThrAlaGlyAlaGlyAlaGlyAspProAlaAlaGly---------ProArgLeuLeu 522

Qy       564 CCTCAGCAGCTGGGCTTGCCTGTGGAGGGAGTGACTTGCACTGGCAGCACTGCATGTCAC 623
Db       523 ProAlaGlyThrGlyAlaProValAlaAlaLeuArg---ThrGlyAlaGlySerAlaGly 541

Qy       624 CTGGGAACCCCTGCAGACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACG 683
Db       542 ArgAla-ProIleGlyThrGlyArgThrLeuGln------ArgArgGlySerArgArgAr 559

Qy       684 TGCAATAATGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTC 743
Db       559 gSer-----------------------------------------AlaAlaAlaArgAl 565

Qy       744 CTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCT 803
Db       565 aAlaArgHisSerArgGlyAlaGlyAlaAlaAspAlaAlaLeuArgSerAlaHisGlyTy 585

Qy       804 CAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCC 863
Db       585 rArgArgVal------------ProValProLeuArgThrIleAlaPro-GlyProAlaA 601

Qy       864 ATCACTGTGTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATG 923
Db       601 spProAlaGlnArgProGlyAlaGlyGlyAlaAlaArgProAlaThrAlaAlaAla---A 620

Qy       924 CCACAGCAGGC--------------------------GGTGGGGGCTGCGTGGGGACAA 956
Db       620 laThrAlaGlySerProAlaAlaThrValArgArgProAlaGlyGlyArgArgGlyGlyA 640

Qy       957 TCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGGGGATGCTCC 1016
Db       640 laGlnSerAlaGlnLeuSerGlyAlaGlyGlyAlaArgProAspArgProGlyLeuLeuG 660

Qy      1017 AGGATGTGGGTGATTCTGTACCTGGGGAG------GCTATCTCTGACCTCCCGACA---G 1067
Db       660 ln------------------ProGlyAspArgArgAlaThrValHisPheProAlaHisG 674

Qy      1068 GGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCA 1127
Db       674 lyGluAspProArgProAlaAspGlnArgGlnAlaArgGlyGlyProSer---------- 690

Qy      1128 AGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG 1187
Db       691 ----------------------------AspProGlyGlyGlyAlaGlyGlnGlyProA 701

Qy      1188 GGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC 1247
Db       701 rgProAla--------------------ProProGluArgProGlnCysArgAlaArgP 714

Qy      1248 CCCTT 1252
Db       714 roVal 715

RESULT 2
US-09-252-991A-17588
; Sequence 17588, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 17588
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17588

Alignment Scores:
Pred. No.:                0.000218        Length:          299
Score:                    126.50          Matches:         94
Percent Similarity:       33.86%          Conservative:    35
Best Local Similarity:    24.67%          Mismatches:      132
Query Match:              4.94%           Indels:          120
DB:                       4               Gaps:            22

US-09-989-919-15 (1-1397) x US-09-252-991A-17588 (1-299)

Qy      1182 CCCACCCCCGCCCCAGGTCCTGGCTCAAACCACACCTGCTCCCTGACCCCAGTCTTGGCT 1123
Db         3 ProSerSerLeuProCysProTrpArgProGlyThrCys---------------------- 15

Qy      1122 CATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGGGCTGGCCTGGGAGTGTCCCCTGTC 1063
Db        16 ------------CysTrpProArgProSerProTrpProPro------------------ 25

Qy      1062 GGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCACCCACATCC--------------- 1018
Db        26 ---------------AlaAlaPro------AspCysProThrSerAlaTrpProArgArg 38

Qy      1017 ---TGGAGCATC---------------CCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGA 976
Db        39 ProTrpSerAlaAlaThrSerProProProArgAlaThrThrArgPro------------ 54

Qy       975 GAGAACACTCCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTGGCATGTGCA 916
Db        55 ------TrpProArgTrpValThrProThr---ProArgSerAlaSerProThrCysArg 71

Qy       915 GCAGCAGCAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACACAGTGATGGGGCTGC 856
Db        72 SerProAlaAlaThrAlaProSerArg------------------------------- 80

Qy       855 CCACGG----------------------AACCGTCCCAGGGAGGGGCACAGCCCCCAG 820
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Db         81 ProArgProLysSerSerThrAlaArgProArgArgProArgArgGly---------- 96

Qy        819 TGGGGAGACTAGCCTGAGCTTGCTTACAGCCCACAGGGTTGGAGAGGCAGTCATACCCCC 760

Db         97 ----------ProAlaArgAlaLeuAla---SerGlyTrpArgProSerProAlaPro 111

Qy        759 ATGATTCCTGGACTAGGAGCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAAC 700

Db        112 AlaThrProSerThrAlaArgProSerAlaCysSerAlaArgProSerAsnArgAlaArg 131

Qy        699 ATTTGGCATTATTGCACGTTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGT 640

Db        132 ThrValProTrpCys--------------ArgSerSerCysSerThrCys-SerThrAr 146

Qy        639 CTGCAGGGGTTCCCAGGTGACATGCAGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCA 580

Db        146 gSerProGlyArgLysSerThrArgSerSerAlaSerThrSerGlyAla---------Ar 163

Qy        579 AGCCCAGCTGCTGAGGATAGTCAGCTGG------TCAGCCGAGCCCTCAGATAGGTCAGC 526

Db        163 gAlaAspCysArgArg---ProThrTrpArgArgSerSerSerThrAlaProArgAlaPr 182

Qy        525 CAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGCTCCATCCAGTCT 466

Db        182 o---------------------------------------------ThrProSer----- 185

Qy        465 TGAAAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGAGGTAACAGGGCTGGATGTTT 406

Db        186 -------------------ThrTrpAlaArgSerSerArgSerAlaSerAlaGlyCysGl 199

Qy        405 CTCTTTC-----------------TGGAGGCAAGACCATTCTCCCTAATTTGACTGCCT 364

Db        199 yAlaTrpMetCysAlaGlyThrAsnTrp-ProArgSerThrArgCysArgAlaThrArg- 218

Qy        363 TGAAGACACGTATACCTCTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGATGGGGGA 304

Db        219 --LysSerArgArgSerCysSerAsn-SerCysAlaProPro---ThrArgProAlaGly 236

Qy        303 TCACTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCC------CTTGGAAGGGCTTCT 250

Db        237 CysProAlaSerGlySerThrArgTrpProGlyCysSerProThrAlaAsnSerAlaSer 256

Qy        249 CCCACTGGCTCACCTGTCCAGGTGGTCTGGTTGGTGACCACAAAGGCCCGA--------- 199

Db        257 ProThrArgArgProProArgArgCysTrpLysArgSerArgArgAlaThrProArgPro 276

Qy        198 CACTGGGCATGGCTCTCACAGACATCCACAGCCTCAGCCAGGTTGAACACTGAAAGG 142

Db        277 GlySerAlaTrpProSerCysSerThrThrIleProThrArgAlaThrTrpLysArg 295

RESULT 3
US-08-026-138E-3
; Sequence 3, Application US/08026138E
; Patent No. 5502166
;  GENERAL INFORMATION:
;    APPLICANT:  Masayoshi MISHINA
;    TITLE OF INVENTION:  NOVEL PROTEINS AND GENES CODING THE SAME
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nishiohata Residence 1-107
;      STREET:  5214, Nishiohata-machi
;      CITY:  Niigata-shi
;      STATE:  Niigata-ken
;      COUNTRY:  JAPAN
;      ZIP:  951
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44 MB storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS v.5
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/026,138E
;      FILING DATE:  26-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 39563/1992
;      FILING DATE:  26-FEB-1992
;      APPLICATION NUMBER:  JP 173155/1992
;      FILING DATE:  30-JUN-1992
;      APPLICATION NUMBER:  JP 215017/1992
;      FILING DATE:  12-AUG-1992
;      APPLICATION NUMBER:  JP 303878/1992
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamburg, C.Bruce
;      REGISTRATION NUMBER:  22,389
;      REFERENCE/DOCKET NUMBER:  F-4551
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 986-2340
;      TELEFAX:  (212) 953-7733
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1239 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single strand
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  mouse
;      TISSUE TYPE:  brain
;    PUBLICATION INFORMATION:
;      AUTHORS:  Masayoshi MISHINA
;      TITLE:  NOVEL PROTEINS AND GENES CODING THE SAME
;      RELEVANT RESIDUES IN SEQ ID NO:  3: FROM 1 to 1239
US-08-026-138E-3

Alignment Scores:
Pred. No.:                0.000736      Length:          1239
Score:                    124.00        Matches:         94
Percent Similarity:       30.63%        Conservative:    23
Best Local Similarity:    24.61%        Mismatches:      112
Query Match:              4.84%         Indels:          153
DB:                       1             Gaps:            24

US-09-989-919-15 (1-1397) x US-08-026-138E-3 (1-1239)

Qy      1196 AGAAAGGCCCCGGCCCCACCCCCGCCCCAGGTCCTGGCTCAAACCACACCTGCTCCCTGA 1137

Db       927 ArgArgAlaProAlaPro-----------------------ThrThrSerGlyPro--- 937

Qy      1136 CCCCAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGGG--------- 1086

Db       938 ------------------ArgSerCysThrProGlyPro------ProGlyGlnProSer 949

Qy      1085 ---CTGGCCTGGGAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAGAAT 1029

Db       950 ProSerGlyTrpArgProPro------GlyGlyGlyArg---ThrProLeuAlaArgArg 966

Qy      1028 CACCCACATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACA 969

Db       967 AlaProGlnProProAlaArgPro------GlyProAlaGln------------------ 978

Qy       968 CTCCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTGGCATGTGCAGCAGCAG 909

Db       979 ------GlyArgLeuSerProThrCysProGluHis------------------------ 988

Qy       908 CAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACACAGTGATGGGGCTGCCCACGGA 849

Db       989 ------------------ProAlaGlyThrLeuGlyMetArgGlyGlyGlnCysGluSer 1002

Qy       848 ACCGTCCCAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCCTG---------AGCTTG 798

Db      1003 GlyIleArgAspArgThrSerArgProProGluArgArgAlaLeuProGluArgSerLeu 1022

Qy       797 CTTACAGCCCAC----------------------------AGGGTTGGAGAGGCAGTC 768

Db      1023 LeuHisAlaHisCysHisTyrSerSerPheProArgAlaGluArgSerGlyArgProPhe 1042
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Qy        767 ATACCCCCATGATTCCTGGACTAGGAGCCAGCA-----------GTCCCATAGCTAGGC 720
              :::|||         |||      ||||||               :::|||   ||||||
Db       1043 LeuPro---------LeuPheProGluProProGluProAspAspLeuProLeuLeuGly 1059

Qy        719 TGGTAAACTCACATTTTAACATTTGGCATTATTGCACGTTTGTCCTGGTCACATCTGTCT 660
                  :::          :::   |||   :::|||:::
Db       1060 ---ProGluGlnLeuAlaArgArgGluAlaLeuLeuArgAlaAlaTrpAla--------- 1075

Qy        659 GTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGG---TGACATGCAGTGCTGCCAGT 603
                                  |||||| ||||||      ||||||   ||||||
Db       1076 ------------------------ArgGly-ProArgProArgHisAlaSerLeuProSe 1087

Qy        602 GCAAGTC------------ACTCCCTCCACAGGCAAGCCCAGC---TGCTGAGGATAGTC 558
                |||             |||   |||          |||:::   |||   |||   ::
Db       1087 rSerValAlaGluAlaPheThrArgSerAsnProLeuProAlaArgCysThrGlyHisAl 1107

Qy        557 AGCTGGTCAGCCGAGCCCTCAGATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTT 498
              :       |||  ||||||
Db       1107 aCysAlaCysProCysProGln----------------------------------- 1114

Qy        497 GGGATCAGGGACCACTTGGCTCCATCCAGTCTTGAAAAAGACCAGCTGCCGA-------- 446
                                                :::   |||||||||
Db       1115 --------------------------------SerArgProSerCysArgHisValAl 1123

Qy        445 ----------------------CCTGGGGGGCAGAGGTGAGAGGTAACAGGGCTGGATGT 408
                                   |||      :::         |||   |||:::
Db       1123 aGlnThrGlnSerLeuArgLeuProSerTyrArgGluAlaCysValGluGlyValProAl 1143

Qy        407 TTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGACTGCCTTGAAGACACGTATACC 348
                :::::                                          |||   ||
Db       1143 aGlyValAlaAla-----------------------------------ThrTrpGlnPr 1151

Qy        347 TCTCTCTCAT---------CACCTCAGCACCCCCTCTGACTTCCGATGGGGGATCACTAT 297
                  |||         |||      |||         |||   ||||||
Db       1151 oArgGlnHisValCysLeuHisThrHisThrHisLeuProPheCysTrpGlyThrValCy 1171

Qy        296 CTATCAACCTCCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCTCCCACTGGCTCAC 237
                  ||||||      |||   |||   ||||||
Db       1171 sArgHisProProProCysSerSerHisSerProTrp---------------------- 1183

Qy        236 CTGTCCAGGTGGTCTGGTTGGT---------------GACCACAAAGGCCCGACACTGGG 192
                        |||:::|||                 |||:::|||   ||||||||
Db       1184 -------------LeuIleGlyThrTrpGluProProSerHisArgGlyArgThrLeuGl 1199

Qy        191 CATG 188
              |:::
Db       1199 yLeu 1200
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RESULT 4
US-09-252-991A-20570
; Sequence 20570, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20570
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (250)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.

US-09-252-991A-20570

Alignment Scores:

Pred. No.:	0.0012	Length:	439
Score:	120.00	Matches:	107
Percent Similarity:	29.48%	Conservative:	23
Best Local Similarity:	24.26%	Mismatches:	146
Query Match:	4.75%	Indels:	165
DB:	4	Gaps:	25

US-09-989-919-15 (1-1397) x US-09-252-991A-20570 (1-439)

```
Qy         16 CCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTAT 75
              |||   |||      :::||||||||||||         :::   |||:::
Db         77 ProHisArgProAspAlaAlaGluLeuHisArgAlaHisArgGlnArgLeuSerAlaLeu 96

Qy         76 CCCAGA---------CAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCA 126
              ||||||         :::   |||||||||            |||   |||   ||||||
Db         97 ProArgGlyAspProArgGlnHisProPro---------ArgLeuGlyAlaAspLeuPro 113

Qy        127 CCACGGGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAG 186
                    ||||||         ::::::|||
Db        114 ------ThrLeuProThrProGlyLeuArgPro-------------------------- 122

Qy        187 CCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGAGCCAGT 246
                        |||           |||:::|||          |||
Db        123 --------------GlyArgAlaArgHisArgProGlyArg-HisGlyGlyGlyAspAl 137

Qy        247 GGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAGATAGTGATCC 306
              |||      |||||:::      |||   |||||||||      |||
Db        137 aAlaGluHis---ProArgAspAlaArgGlyAlaLeuTrpArgAlaAspAsp-------- 153

Qy        307 CCCATCGGAAGTCAGAGGGGGTGCTGAG-----------GTGATGAGAGAGAGGTATAC 354
                        |||   |||||||||                |||   |||
Db        154 ------------ArgArgGlyAlaGluHisProGlnArgThrProArgArgArgSerHi 169

Qy        355 GTGTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGA------AA 408
              |||      :::      |||      |||         |||   |||
Db        169 sArgLeuHisAlaAlaThrArgArgSerGlnGlyAlaAspHisArgLeuArgIleProAr 189

Qy        409 CATCCAGCCCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGA 468
              ||||||                  |||   :::|||   |||       |||
Db        189 gGlyAspProCysArgHisArgTyrAlaArgProProAlaAlaGlyGlyArgArgGlnAr 209

Qy        469 C---------TGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGG 519
                      |||      |||   |||
Db        209 gProArgValTrpArgArgProProGly------------------------------- 218

Qy        520 CCTCTGGCTGACCTATCTG--------------AGGGCTCGGCTGACCAGCTGACTATC 564
              |||   |||   |||                  |||   |||                |||
Db        219 ----TrpArgThrGlyLeuArgGlyAlaAlaArgArgGlyArgProAlaValArgLeuGl 237

Qy        565 CTCAGCAGCTGGGCTTGCCTGTGGAGGG---AGTGACTTGCACTGGCAGCACTGCATGTC 621
              |||   |||          |||      ::::::   |||       |||
Db        237 yMetAlaProGlyArgValAlaGlyAspLeuAlaGlu***HisLeuGlyHisHisArgGl 257

Qy        622 ACCT--------------GGGAACCCCTGCAGACAAAGCTAACATCCCAGACAGACAGA 666
               |||                ::|||   |||                  |||   ||
Db        257 nProGlnGlyArgGlyLeuProSerProArgArgLeuProGluArgAlaGlyGlnProAs 277

Qy        667 TGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGC 726
              |                                                    |||
Db        277 p-------------------------------------------------AspLeuVa 280

Qy        727 TATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTG 786
              |||      |||:::||||||:::                  ||||||   |||
Db        280 lHisGly---------ProAlaProGlyVal--------------ProLeuAspProAl 292

Qy        787 TGGGCTGTAAGCAAGC----------------------------TCAGGCTAGTCTCC 816
              :::                                      :::|||     ||
Db        292 aAspValProLeuGlnArgLeuValLeuSerValAspGlyAspArgAlaGlyArgPr 312

Qy        817 CCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCA 876
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Db        312 oArg---------LeuProAlaAlaGlyArgSerAlaLysGlyProHis---------- 325

Qy        877 ATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCA---------------- 919
                                 :::||||||
Db        326 ----------ProAspProArgAlaProGlyGlnProProValArgArgAlaHisArgAl 342

Qy        920 ----------------CATGCCACAGCAGGC-----------------GGTGGGGGCTG 945
                           ||||||      |||                   |||   ||
Db        342 aGlnArgProAspGlnHisAlaArgPheGlyGlnGlyArgHisArgProProGlyAlaCy 362

Qy        946 CGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCG 1005
              |   |||         |||                 :::||||||          ||
Db        362 sHisGlyArgArgArgArgAla-----------------ThrGlyGlnGlyAspArgAr 376

Qy       1006 GGGG---------------------------------------------------------- 1009
              ||||
Db        376 gGlyGlyArgAspGlyHisProArgHisProCysLeuArgProHisArgGlyLeuArgPr 396

Qy       1010 ----------------ATGCTCCAGGATGTGGGT------------------------- 1027
                             :::   :::   ||||||
Db        396 oGlyHisGlyLeuArgLeuAlaArgArgValGlyArgProAlaAlaGlyAlaThrArgAr 416

Qy       1028 -GATTCTGTA---CCTGGGGAGGCTATCTCTGACCTCCCGACAGGGGACACTCCCAGGCC 1083
               |||   |||   ||||||  |||:::  |||         ||||||     |||||
Db        416 gAspGlnValAlaProGlyArgAlaLeuProAspProArgArgGlyAspGlyGlyArgPr 436

Qy       1084 A 1084
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Db        436 o 436
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RESULT 5
US-09-467-997-1
; Sequence 1, Application US/09467997
; Patent No. 6379925
; GENERAL INFORMATION:
; APPLICANT: Kitajewski, Jan
; APPLICANT: Uyttendaele, Hendrik
; TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
; FILE REFERENCE: 53863-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/467,997
; CURRENT FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1964
; TYPE: PRT
; ORGANISM: mouse
US-09-467-997-1

Alignment Scores:

Pred. No.:	0.00232	Length:	1964
Score:	120.00	Matches:	128
Percent Similarity:	28.72%	Conservative:	38
Best Local Similarity:	22.15%	Mismatches:	193
Query Match:	4.75%	Indels:	220
DB:	4	Gaps:	36

US-09-989-919-15 (1-1397) x US-09-467-997-1 (1-1964)

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Qy          6 TGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGG------CAAGCAGCAGTA 59
              |||      ||||||:::         ||||||   |||         |||      :::
Db        903 CysIleAspThrGlySerSerTyrPheCysArgCysProProGlyPheGlnGlyLysLeu 922

Qy         60 CCGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAG---------------------- 97
                    :::|||:::      |||:::|||
Db        923 CysGlnAspAsnValAsnProCysGluProAsnProCysHisHisGlySerThrCysVal 942

Qy         98 ---------GAAGACTAC------CGCTGCTGGCCATCCTACCACCACGGGAGCTGCCTC 142
                      |||      :::|||   |||   |||         :::|||
Db        943 ProGlnProSerGlyTyrValCysGlnCysAlaProGlyTyrGluGlyGlnAsnCys--- 961

Qy        143 CTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCCAGTGTCGG 202
```

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Db        962 -----------------SerLysValLeuAspAlaCysGlnSerGln---ProCysHis 974

Qy        203 GCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGAGCCAGTGGGAGAA------GCC 256
                          |||      |||   |||      |||   |||         |||
Db        975 --------------AsnHisGlyThrCysThrSerArgProGlyGlyPheHisCysAla 989

Qy        257 CTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTG----------ATAGATAGT------ 301
                |||              |||         |||            :::|||
Db        990 CysProProGlyPheValGly------LeuArgCysGluGlyAspValAspGluCysLeu 1007

Qy        302 GATCCCCCATCGGAAGTCAGAGGGGGTGCT---------GAGGTGATGAGAGAGAGGTAT 352
              |||   |||               |||   |||          :::          |||
Db       1008 AspArgProCysHisProSerGlyThrAlaAlaCysHisSerLeuAlaAsnAlaPheTyr 1027

Qy        353 ---ACGTGTCTTCAAGGC------------------------------------------ 367
                 ||||||   |||
Db       1028 CysGlnCysLeuProGlyHisThrGlyGlnArgCysGluValGluMetAspLeuCysGln 1047

Qy        368 AGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGCCCT------GT 421
              ||||||         ||||||   :::    |||       |||       |||
Db       1048 SerGlnProCysSerAsnGlyGlySerCys-GluIleThrThrGlyProProProGlyPh 1067

Qy        422 TACCTCTCACCTCTGCCCCCCAGGTCGGCAG---------------------------- 452
               |||   |||   ||||||   |||  :::
Db       1067 eThrCysHis---CysProLysGlyPheGluGlyProThrCysSerHisLysAlaLeuSe 1086

Qy        453 ----CTGGTCTTTTTCAAGACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCAC 508
                  :::                                 :::|||   |||
Db       1086 rCysGlyIleHisHisCysHisAsnGlyGlyLeuCysLeuProSerPro----------- 1102

Qy        509 ATATGTGAAGGCCTCTGGCTGACCT-----------ATCTGAGGGCTCGGCTGACCA-- 554
                 |||           |||           :::   |||   |||   |||
Db       1103 -------LysProGlySerProProLeuCysAlaCysLeuSerGlyPheGlyGlyProAs 1120

Qy        555 ----------GCTGACTATCCTCAGCAGCTGGGCTTGCCT---------GTGGAGGGAGT 595
                             |||       |||  |||         :::
Db       1120 pCysLeuThrProProAlaProProGlyCysGlyProProSerProCysSerLeuHisAsnGl 1140

Qy        596 GACTTGCACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCAGACAAAGCTAACATCCC 655
              |||||||||   :::           ||||||   |||       :::         ||
Db       1140 yThrCysThrGluThrProGly------LeuGlyAsnProGlyPheGlnCysThrCysPr 1158

Qy        656 AGACAGACAGATGTGACCAGGACAAACGTGCAAT------------------------- 689
              |                |||||     |||
Db       1158 oProAspSer------ProGlyProArgCysGlnArgProGlyAlaSerGlyCysGluGl 1176

Qy        690 ----------------------AATGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCT 727
                                   :::|||   |||         |||   |||
Db       1176 yArgGlyGlyAspGlyThrCysAspAlaGlyCys---------SerGlyProGlyGlyAs 1193

Qy        728 ATGGGAC---------------------------------------------------- 734
              |||||
Db       1193 pTrpAspGlyGlyAspCysSerLeuGlyValProAspProTrpLysGlyCysProProHi 1213

Qy        735 -------TGCTGGCTCCTAGTCCAGGAATCATGG------------------------- 761
                    ||||||||||||   ::::::
Db       1213 sSerGlnCysTrpLeuLeuPheArgAspGlyArgCysHisProGlnCysAspSerGluGl 1233

Qy        762 -------------GGGTATGACTGCCTCTCCAACCCTGTG------------------- 788
                          ||||||||||||         |||
Db       1233 uCysLeuPheAspGlyTyrAspCysGluIleProProThrCysIleProAlaTyrAspGl 1253

Qy        789 ------------------------------------GGCTGTAAGCAAGCTCAGGC 808
                                                  ||||||    |||:::
Db       1253 nTyrCysArgAspHisPheHisAsnGlyHisCysGluLysGlyCysAsnAsnAlaGluCy 1273

Qy        809 TAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCAC 868
                    |||   |||   |||      :::   |||   |||   |||
Db       1273 sGlyTrpAspGlyGlyAspCysArgProGluGlyGluAspSerGluGlyArgProSerLe 1293

Qy        869 TGTGTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCACA 928
                                              ||||||::::::|||      |||
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Db       1293 uAla----------------------------LeuLeuValValLeuArgProPro-- 1302

Qy        929 GCAGGCGGTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCT 988

Db       1303 ----------------AlaLeuAspGlnGlnLeuLeuAlaLeuAlaArgValLeuSerLe 1317

Qy        989 GGACAGGAGACTTGGCGGGGGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCT 1048

Db       1317 uThrLeuArgValGly--------------LeuTrpVal--------------ArgLy 1327

Qy       1049 ATCTCTGACCTCCCGACAGGGGACACTCCCA---------------------------- 1079

Db       1327 sAspSerGluGlyArgAsnMetValPheProTyrProGlyThrArgAlaLysGluGluLe 1347

Qy       1080 -------GGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCA----- 1127

Db       1347 uSerGlyAlaArgAspSerSerSerTrpGluArgGlnAlaProProThrGlnProLeuGl 1367

Qy       1128 -------------AGACTGGGGTCAGGG--------------------------AGCAG 1147

Db       1367 yLysGluThrGluSerLeuGlyAlaGlyPheValValValMetGlyValAspLeuSerAr 1387

Qy       1148 GTGTGGTTTGAGCCAGGACCTGGGGCGG---GGGTGGGGCCGGGGCCTTTCTGCCTCATT 1204

Db       1387 gCysGlyProGluHisProAlaSerArgCysProTrpAspSerGlyLeuLeuLeuArgPh 1407

Qy       1205 TGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTC 1256

Db       1407 eLeu---------AlaAlaMetAlaAlaValGlyAlaLeuGluProLeuLeu 1421

RESULT 6
US-08-093-453B-3
; Sequence 3, Application US/08093453B
; Patent No. 5439814
;  GENERAL INFORMATION:
;    APPLICANT:  Frey, Teryl K.
;    APPLICANT:  Dominguez, Geraldina
;    APPLICANT:  Wang, Chin_Yen
;    TITLE OF INVENTION:  Modified Infectious Rubella Virus
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jamie L. Greene, Jones & Askew
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  United States
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50
;      COMPUTER:  MacIntosh
;      OPERATING SYSTEM:  7.0
;      SOFTWARE:  Microsoft Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/093,453B
;      FILING DATE:  19 JUL 1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.S. 07/722,334
;      FILING DATE:  28 JUN 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Greene, Jamie L.
;      REGISTRATION NUMBER:  32,467
;      REFERENCE/DOCKET NUMBER:  07362-0101
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404_818-3700
;      TELEFAX:  404_818-3799
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1063 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  C_terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rubella virus
;      STRAIN:  Therien
US-08-093-453B-3

Alignment Scores:
Pred. No.:                0.00224        Length:          1063
Score:                    119.00         Matches:         96
Percent Similarity:       31.65%         Conservative:    36
Best Local Similarity:    23.02%         Mismatches:      136
Query Match:              4.65%          Indels:          149
DB:                       1              Gaps:            20

US-09-989-919-15 (1-1397) x US-08-093-453B-3 (1-1063)

Qy       1184 GCCCCACCCCCGCCCCAGGTCCTGGCTCAAACC---------ACACCTGCTCCCTGACCC 1134

Db         77 AlaProProProProGluGluArgGlnGluThrArgSerGlnThrProAlaProLysPro 96

Qy       1133 CAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGGGCTGGCCTGGGAG 1074

Db         97 SerArg-----------------AlaPro---ProGlnGlnProGln------------ 105

Qy       1073 TGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAG--------------AAT 1029

Db        106 --------------------------ProProArgMetGlnThrGlyArgGlyGlySer 116

Qy       1028 CACCCACATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGA--- 972

Db        117 AlaProArgProGluLeuGlyProProThrAsnProPheGlnAlaAlaValAlaArgGly 136

Qy        971 ---------ACACTCCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGT----- 926

Db        137 LeuArgProProLeuHisAspPro---AspThrGlu-AlaProThrGluAlaCysValTh 155

Qy        925 ----GGCATGTGCAGCAGCAGCAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACAC 870

Db        155 rSerTrpLeuTrpSerGluGlyGluGlyAlaValPheTyrArgValAspLeuHisPheTh 175

Qy        869 AGTGATGGGGCTGCCCACGGAACCGTCCCAGGGA-------------------------- 836

Db        175 rAsnLeuGlyThrProProLeuAspGluAspGlyArgTrpAspProAlaLeuMetTyrAs 195

Qy        835 -------GGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCACAGG 783

Db        195 nProCysGlyProGluProPro---AlaHisValValArgAlaTyrAsnGlnProAlaGl 214

Qy        782 GTTGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGAGCCAGCAGTCCCATAGCTA 723

Db        214 yAspValArgGlyValTrpGlyLysGlyGluArgThrTyrAlaGluGlnAspPheArgVa 234

Qy        722 GGCTGGTAAACTCACATTTTAACATTTGGCATTATTGCACGTTTGTCCTGGTCACATCTG 663

Db        234 lGlyGly------ThrArgTrpHisArgLeuLeu-----------------ArgMetPr 246

Qy        662 TCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGTGACATGCAGTGCTGCCAGT 603

Db        246 oValArgGlyLeuAspGlyAspSerAlaProLeuProPro---HisThrThrGluArgIl 265

Qy        602 GCAAGTCACTCCCTCCACAGGCAAGCCCAGCTGCTGAGGATAGTCAGCTGGTCAGCCG-- 545

Db        265 eGluThrArg--------------------------------SerAlaArgHisProTr 274

Qy        544 -AGCCCTCAGATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGAC 486

Db        274 pArgIleArgPheGlyAlaProGlnAlaPheLeuAlaGlyLeuLeuLeuAlaThrValAl 294

Qy        485 CACTTGGCTCCATCCAGTCTTGAAAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGA 426

Db        294 a-ValGlyThrAlaArgAlaGlyLeuGlnProArgAlaAspMet---------------- 308
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Qy        425 GGTAACAGGGCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGACTGC 366

Db        308 ------------------------------------------------------------ 308

Qy        365 CTTGAAGACACGTATACCTCTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGATGGGG 306

Db        309 ------------------------------AlaAlaProProThr-LeuProGlnPro 317

Qy        305 GATCACTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCTCCCA 246

Db        318 ------------------------------------------------------------Pro 318

Qy        245 CTGGCTCACCTGTCCAGGTGGTCTGGTTGGTGACCACAAAGGCCCGACACTGGGCATGGC 186

Db        319 CysAlaHisGlyGlnHisTyrGlyHisHisHisHisGlnLeuProPheLeuGlyHisAsp 338

Qy        185 TCTCACAGACATCCACAGCCTCAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCGTGGT 126

Db        339 GlyHisHis------------------------------GlyGlyThrLeuArgVal 347

Qy        125 GGTAGGATGGCCAGCAGCGGTAGT--------------------CTTCCTGGGGGATGG 87

Db        348 GlyGlnHisTyrArgAsnAlaSerAspValLeuProGlyHisTrpLeuGlnGlyGlyTrp 367

Qy         86 TGCTGTCTGGGA------------TACACTGGTACTCGGTACTGC 54

Db        368 GlyCysTyrAsnLeuSerAspTrpHisGlnGlyThrHisValCys 382

RESULT 7
US-07-960-389-2
; Sequence 2, Application US/07960389
; Patent No. 5705611
;  GENERAL INFORMATION:
;    APPLICANT:  HAYASHIDA, Kasuhiro;
;    TITLE OF INVENTION:  Human GM-CSF Receptor Component
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering-Plough Corporation
;      STREET:  2000 Galloping Hill Road
;      CITY:  Kenilworth
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07033
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disc
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  System Software 7.1
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/960,389
;      FILING DATE:  07-JAN-1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  554,745
;      FILING DATE:  18-JUL-1990
;      APPLICATION NUMBER:  PCT/US 91/04846
;      FILING DATE:  16-JUL-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Blasdale, John H. C.
;      REGISTRATION NUMBER:  31,895
;      REFERENCE/DOCKET NUMBER:  DX0143Q
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908) 298-2902
;      TELEFAX:  (908) 298-5388
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  897 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      OTHER INFORMATION:  Human GM-CSF receptor;  Signal Sequence:  -17 to -1;  Transme
US-07-960-389-2

Alignment Scores:
Pred. No.:                0.00263        Length:          897
Score:                    118.00         Matches:         104
Percent Similarity:       34.37%         Conservative:    51
Best Local Similarity:    23.06%         Mismatches:      152
Query Match:              4.61%          Indels:          144
DB:                       1              Gaps:            22

US-09-989-919-15 (1-1397) x US-07-960-389-2 (1-897)

Qy       1221 GGCTTTCATTGAAAGCAAATGAGGCAGAAAGGCCCCGGCCCCACCCCCGCCCCAGGTCCT 1162

Db        464 GlyIleTyrGlyTyrArgLeuArgArgLysTrpGluGluLysIleProAsnProSerLys 483

Qy       1161 GGC---------TCAAACCACACCTGCTCCCTGACCCCAGTCTTGGCTCATGCTGAGGTG 1111

Db        484 SerHisLeuPheGlnAsnGlySerAlaGluLeuTrpProProGlySerMetSerAlaPhe 503

Qy       1110 TGCACCTCTGCCCCT---------GACCCCTGGGCTGGCCTG--------------GGA 1075

Db        504 ThrSerGlySerProProHisGlnGlyProTrpGlySerArgPheProGluLeuGluGly 523

Qy       1074 GTGTCCCCTGTC------GGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCACCCACA 1021

Db        524 ValPheProValGlyPheGlyAspSerGluVal----------------SerProLeu 537

Qy       1020 TCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACACTCCACGA 961

Db        538 ThrIleGluAspProLysHisValCysAspProProSerGlyProAspThrThrProAla 557

Qy        960 TGGATT---GTCCCCACG----------------CAGCCCCCACCGCCTGCTGTGGCA 922

Db        558 AlaSerAspLeuProThrGluGlnProProSerProGlnProGlyProProAlaAlaSer 577

Qy        921 TGTGCAGCAGCAGCAGCAGGGGCTTTAGCTA---------------------------- 891

Db        578 HisThr-ProGluLysGlnAlaSerSerPheAspPheAsnGlyProTyrLeuGlyProPr 597

Qy        890 -CATTCTCACACTATTGAACACAGTGATGGGGCTGCCCACGGAACCGTCCCAGGGAGGGG 832

Db        597 oHisSerArgSer-LeuProAspIleLeuGlyGlnProGluProProGlnGluGlyGlyS 617

Qy        831 CACAG------CCCCCAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCACAGGGTTGG 778

Db        617 erGlnLysSerProProProGlySerLeuGluTyrLeuCysLeu---ProAlaGlyGlyG 636

Qy        777 AGAGGCAGTCATACCCCCATGATTCCTGGACTAGGAGCCAGCAGTCCCATAGCTAGGCTG 718

Db        636 lnValGlnLeuValPro---------------------------------------- 641

Qy        717 GTAAACTCACATTTTAACATTTGGCATTATTGCACGTTTGTCCTGGTCACATCTGTCTGT 658

Db        641 ------------------------------------------------------------ 641

Qy        657 CTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGTGACATGCAGTGCTGCCAGTGCAAG 598

Db        642 --------LeuAlaGlnAlaMetGlyProGlyGln---------AlaValGluValGluA 656

Qy        597 TCACTCCCTCCACAGGCAAGCCCAGCTGCTGAGGATAGTCAGCTGGTCAGCCGAGCCCTC 538

Db        656 rgArgProSerGlnGly--------------------AlaAlaGlySerProSerLeuG 669

Qy        537 AGATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGC 478

Db        669 luSerGlyGly------------------------------GlyProAlaProProAlaL 679

Qy        477 TCCATCCAGTCTTGAAAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGAGGTAACAG 418

Db        679 euGlyPro--------------------ArgValGlyGlyGlnAspGlnLysAspSerP 692
```

```
Qy        417 GGCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGACTGCCTTGAAGA 358
Db        692 roValAlaIleProMetSerSerGlyAspThrGluAspProGlyValAlaSerGlyTyrV 712

Qy        357 CACGTATACCTCTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGATGGGGGATCACTA 298
Db        712 alSer-SerAlaAspLeuVal--------------PheThrProAsnSerGlyAlaSer 726

Qy        297 TCTATCAACCTC----------------------CAGAGAGGTCCTGCCATCTCCCTT 262
Db        727 SerValSerLeuValProSerLeuGlyLeuProSerAspGlnThrProSerLeuCysPro 746

Qy        261 GGAAGGGCTTCT---CCCACTGGCTCACCTGTCCAGGTG---------------------- 226
Db        747 GlyLeuAlaSerGlyProProGlyAlaProGlyProValLysSerGlyPheGluGlyTyr 766

Qy        225 GTCTGGTTGGTGACCACAAAGGCCCGACACTGGGCATGGCTCTCACAGACATCCACAGCC 166
Db        767 ValGluLeuProProIleGluGlyArg-SerProArgSerProArgAsnAsnProValPr 786

Qy        165 T----------------------CAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCG 130
Db        786 oProGluAlaLysSerProValLeuAsnProGly--------------------GluAr 799

Qy        129 TGGTGGTAGGATGGCCAGCAGCGGTAGTCTTCCTGGGGGATGGTGCTGTCTGGGATACAC 70
Db        799 gProAlaAspValSerProThrSerProGlnProGluGlyLeuLeuValLeuGlnGlnVa 819

Qy         69 TGGTACTCGGTACTGCTGCTTGCCG 45
Db        819 lGlyAsp---TyrCysPheLeuPro 826
```

RESULT 8
US-09-266-225D-18
; Sequence 18, Application US/09266225D
; Patent No. 6573364
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishan
; APPLICANT: Kingsmore, Stephen
; APPLICANT: Tchernev, Velizar
; TITLE OF INVENTION: Isolation and Characterization of Hermansky-Pudlak
; TITLE OF INVENTION: Syndrome (HPS) Protein Complexes and HPS Protein-
; TITLE OF INVENTION: Interacting Proteins
; FILE REFERENCE: 15966-523
; CURRENT APPLICATION NUMBER: US/09/266,225D
; CURRENT FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 1184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-266-225D-18

Alignment Scores:

Pred. No.:	0.00377	Length:	1184
Score:	117.00	Matches:	92
Percent Similarity:	32.23%	Conservative:	34
Best Local Similarity:	23.53%	Mismatches:	140
Query Match:	4.57%	Indels:	125
DB:	4	Gaps:	20

US-09-989-919-15 (1-1397) x US-09-266-225D-18 (1-1184)

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Qy       1190 GCCCCGGCCCCACCC---------------------------------------------- 1176
Db        365 AlaProAlaProProMetArgPheProTyrSerSerSerSerSerSerSerAlaAlaAla 384

Qy       1175 --------------------------------CCGCCCCAGGTCCTGGCTCAAACCACA 1149
Db        385 SerSerSerSerSerSerSerSerSerSerAlaSerProPheProAlaSerGlnAlaLeu 404

Qy       1148 CCTGCT--------------CCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGCACCT 1104
Db        405 ProSerTyrProHisSerPheProProProThrSerLeuSerValSerAsnGlnProPro 424

Qy       1103 CTGCCCCTGACCCCTGGGCTGGCCTGGGAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCT 1044
Db        425 LysTyrThrGlnProSerLeuProSerGlnAlaValTrpSerGlnGlyProProProPro 444

Qy       1043 CCCCAG--------------GTACAGAATCACCCACATCCTGGAGCATCCCCCGCCAAG 999
Db        445 ProProTyrGlyArgLeuLeuAlaAsnSerAsnAlaHisProGlyProPheProPro--- 463

Qy        998 TCTCCTGTCCAGACCTAAGCTGAGAGAACACTCCACGATGGATTGTCCCCACGCAGCCCC 939
Db        464 ---------SerThrGlyAlaGlnSerThrAlaHisProProValSerThrHisHisHis 480

Qy        938 CACCGCCTGCTGTGGCATGTGCAGCAGCAGCAGGGGCTTTAGCTACAT--------- 888
Db        481 HisHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnHisHisGlyAsn 500

Qy        887 --------------------------TCTCACACTATTGAACACAGTGATGGGGCTGCC 855
Db        501 SerGlyProProProProGlyAlaPheProHisProLeuGlu------GlyGlySerSer 518

Qy        854 CACGGAACCGTCCCAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTT 795
Db        519 HisHisAlaHisPro---TyrAlaMetSerPro-----------SerLeuGlySerLeu 533

Qy        794 ACAGCCCACAGGGTTGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGAGCCAGCA 735
Db        534 ArgProTyrProProGlyProAlaHisLeuProPro------------------------ 545

Qy        734 GTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGGCATTATTGCACGTTTGTCC 675
Db        546 ---------------------ProHis--------------------SerGlnValSer 551

Qy        674 TGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGTGACATGC 615
Db        552 TyrSerGlnAlaGlyPro--------------------AsnGlyProProValSerSer 564

Qy        614 AGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCAAGCCCAGCTGCTGAGGATAGTCAGC 555
Db        565 SerSerAsnSerSerSer-SerThrSerGlnGlySerTyrProCys-------------- 579

Qy        554 TGGTCAGCCGAGCCCTCAG---------ATAGGTCAGCCAGAGGCCTTCACATATGTGGT 504
Db        580 -SerHisProSerProSerGlnGlyProGlnGlyAlaProTyrProPheProProValPr 599

Qy        503 CTTGTTGGGATCAGGGACCACTTGGCTCCATCCAGTCTTGAAAAAGACCAGCTGCCGACC 444
Db        599 oThrValThrThrSerSerAlaThrLeuSerThrValIleAlaThrValAlaSerSerPr 619

Qy        443 TGGGGGGCAGAGGTGAGAGGTAACAGGGCTGGATGTTTCTCTTTCTGGA----------- 395
Db        619 oAlaGlyTyrLys-----------------ThrAlaSerProProGlyProProProTy 633

Qy        394 -GGCAAGACCATTCTCCCTAATTTGACTGCCTTGAAGACACGTATACCTCTCTCTCATCA 336
Db        633 rGlyLysArg---AlaProSerProGlyAlaTyrLysThrAlaThrProProGlyTyrLy 652

Qy        335 CCTCAGCACCCCCTCTGACTTCCGATGGGGGATCACTATCTATCAACCTCCAGAGAGGTC 276
Db        652 sProGlySerProProSerPheArgThrGly------------ThrProPro-------- 665

Qy        275 CTGCCATCTCCCTTGGAAGGGCTTCTCCCACTGGCTCACCTGTCCAGGTGGTCTGGTTGG 216
Db        666 ----------GlyTyrArgGly--------------ThrSerProProAlaGlyProGl 677

Qy        215 TGACCACAAA------GGCCCGACACTGGGC 191
Db        677 yThrPheLysProGlySerProThrValGly 687
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RESULT 9
US-09-041-886-23

```
; Sequence 23, Application US/09041886
; Patent No. 6235872
;  GENERAL INFORMATION:
;    APPLICANT:  Bredesen, Dale E.
;    APPLICANT:  Rabizadeh, Sharroz
;    TITLE OF INVENTION:  Proapoptotic Peptides, Dependence
;    TITLE OF INVENTION:  Polypeptides and Methods of Use
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/041,886
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-LJ 2626
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1185 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-041-886-23

Alignment Scores:
Pred. No.:                0.00377        Length:          1185
Score:                    117.00         Matches:         92
Percent Similarity:       32.23%         Conservative:    34
Best Local Similarity:    23.53%         Mismatches:      140
Query Match:              4.57%          Indels:          125
DB:                       3              Gaps:            20

US-09-989-919-15 (1-1397) x US-09-041-886-23 (1-1185)

Qy       1190 GCCCCGGCCCCACCC---------------------------------------------- 1176
                ||||||||||||||||
Db        366 AlaProAlaProProMetArgPheProTyrSerSerSerSerSerSerSerAlaAlaAla 385

Qy       1175 --------------------------------CCGCCCCAGGTCCTGGCTCAAACCACA 1149
                                               |||         :::|||
Db        386 SerSerSerSerSerSerSerSerSerSerAlaSerProPheProAlaSerGlnAlaLeu 405

Qy       1148 CCTGCT--------------CCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGCACCT 1104
                |||:::              |||  |||  |||     :::           |||
Db        406 ProSerTyrProHisSerPheProProProThrSerLeuSerValSerAsnGlnProPro 425

Qy       1103 CTGCCCCTGACCCCTGGGCTGGCCTGGGAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCT 1044
                    |||  |||     :::     |||  |||      |||
Db        426 LysTyrThrGlnProSerLeuProSerGlnAlaValTrpSerGlnGlyProProProPro 445

Qy       1043 CCCCAG--------------GTACAGAATCACCCACATCCTGGAGCATCCCCCGCCAAG 999
                |||                    ::::::   |||||||||     |||
Db        446 ProProTyrGlyArgLeuLeuAlaAsnSerAsnAlaHisProGlyProPhePro--- 464

Qy        998 TCTCCTGTCCAGACCTAAGCTGAGAGAACACTCCACGATGGATTGTCCCCACGCAGCCCC 939
                    |||  |||:::  |||  |||     :::|||
Db        465 ---------SerThrGlyAlaGlnSerThrAlaHisProProValSerThrHisHisHis 481

Qy        938 CACCGCCTGCTGTGGCATGTGCAGCAGCAGCAGCAGGGGCTTTAGCTACAT--------- 888
                |||                 ||||||||||||||||      |||
Db        482 HisHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnHisHisGlyAsn 501

Qy        887 --------------------------TCTCACACTATTGAACACAGTGATGGGGCTGCC 855
                                         |||  :::|||       |||::::::
Db        502 SerGlyProProProProGlyAlaProHisProLeuGlu------GlyGlySerSer 519

Qy        854 CACGGAACCGTCCCAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTT 795
                |||      |||          :::|||          ||||||      |||
Db        520 HisHisAlaHisPro---TyrAlaMetSerPro-----------SerLeuGlySerLeu 534

Qy        794 ACAGCCCACAGGGTTGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGAGCCAGCA 735
                  :::      |||  |||  :::||||||
Db        535 ArgProTyrProProGlyProAlaHisLeuProPro---------------------- 546

Qy        734 GTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGGCATTATTGCACGTTTGTCC 675
                                     |||                 :::::::::|||
Db        547 --------------------ProHis-------------------SerGlnValSer 552

Qy        674 TGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGTGACATGC 615
                :::|||                                  |||     |||:::
Db        553 TyrSerGlnAlaGlyPro--------------------AsnGlyProProValSerSer 565

Qy        614 AGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCAAGCCCAGCTGCTGAGGATAGTCAGC 555
                |||:::   |||:::||| :::   |||   |||         |||
Db        566 SerSerAsnSerSerSer-SerThrSerGlnGlySerTyrProCys-------------- 580

Qy        554 TGGTCAGCCGAGCCCTCAG---------ATAGGTCAGCCAGAGGCCTTCACATATGTGGT 504
                  ||||||||                |||   |||      |||      |||
Db        581 -SerHisProSerProSerGlnGlyProGlnGlyAlaProTyrProPheProProValPr 600

Qy        503 CTTGTTGGGATCAGGGACCACTTGGCTCCATCCAGTCTTGAAAAAGACCAGCTGCCGACC 444
                  :::   :::   :::      |||      |||:::         :::      ||
Db        600 oThrValThrThrSerSerAlaThrLeuSerThrValIleAlaThrValAlaSerSerPr 620

Qy        443 TGGGGGGCAGAGGTGAGAGGTAACAGGGCTGGATGTTTCTCTTTCTGGA----------- 395
                |   |||   :::                          |||      |||
Db        620 oAlaGlyTyrLys-----------------ThrAlaSerProProGlyProProProTy 634

Qy        394 -GGCAAGACCATTCTCCCTAATTTGACTGCCTTGAAGACACGTATACCTCTCTCTCATCA 336
                 ||||||         |||:::      |||  ||||||      |||     :::
Db        634 rGlyLysArg---AlaProSerProGlyAlaTyrLysThrAlaThrProProGlyTyrLy 653

Qy        335 CCTCAGCACCCCCTCTGACTTCCGATGGGGGATCACTATCTATCAACCTCCAGAGAGGTC 276
                  :::|||      ||||||  |||               ||||||
Db        653 sProGlySerProProSerPheArgThrGly-----------ThrProPro-------- 666

Qy        275 CTGCCATCTCCCTTGGAAGGGCTTCTCCCACTGGCTCACCTGTCCAGGTGGTCTGGTTGG 216
                          ::::::|||               |||  |||             ||
Db        667 ----------GlyTyrArgGly--------------ThrSerProProAlaGlyProGl 678

Qy        215 TGACCACAAA------GGCCCGACACTGGGC 191
                |    |||      ||||||:::|||
Db        678 yThrPheLysProGlySerProThrValGly 688

RESULT 10
US-09-046-158A-2
; Sequence 2, Application US/09046158A
; Patent No. 6187552
;  GENERAL INFORMATION:
;    APPLICANT:  Roberds, Steven L.
;    APPLICANT:  Kaytes, Paul S.
;    TITLE OF INVENTION:  METHOD FOR IDENTIFYING INHIBITORS OF
;    TITLE OF INVENTION:  JAK2/CYTOKINE RECEPTOR BINDING
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pharmacia & Upjohn Co., Intellectual Property
;      ADDRESSEE:  Legal Services
;      STREET:  301 Henrietta Street
;      CITY:  Kalamazoo
;      STATE:  MI
;      COUNTRY:  USA
```

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;      ZIP:  49001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/046,158A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Darnley Jr., James D.
;      REGISTRATION NUMBER:  33,673
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616/833-2210
;      TELEFAX:  616/833-8897
;      TELEX:  224401
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  433 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-046-158A-2

Alignment Scores:
Pred. No.:              0.00307       Length:          433
Score:                  116.00        Matches:         103
Percent Similarity:     34.30%        Conservative:    50
Best Local Similarity:  23.09%        Mismatches:      149
Query Match:            4.53%         Indels:          144
DB:                     3             Gaps:            22

US-09-989-919-15 (1-1397) x US-09-046-158A-2 (1-433)

Qy       1206 CAAATGAGGCAGAAAGGCCCCGGCCCCACCCCCGCCCCAGGTCCTGGC---------TCA 1156
Db          5 ArgLeuArgArgLysTrpGluGluLysIleProAsnProSerLysSerHisLeuPheGln 24

Qy       1155 AACCACACCTGCTCCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCT 1096
Db         25 AsnGlySerAlaGluLeuTrpProProGlySerMetSerAlaPheThrSerGlySerPro 44

Qy       1095 ---------GACCCCTGGGCTGGCCTG---------------GGAGTGTCCCCTGTC--- 1063
Db         45 ProHisGlnGlyProTrpGlySerArgPheProGluLeuGluGlyValPheProValGly 64

Qy       1062 ---GGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCACCCACATCCTGGAGCATCCCC 1006
Db         65 PheGlyAspSerGluVal-----------------SerProLeuThrIleGluAspPro 78

Qy       1005 CGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACACTCCACGATGGATT---GTCCCC 949
Db         79 LysHisValCysAspProProSerGlyProAspThrThrProAlaAlaSerAspLeuPro 98

Qy        948 ACG-----------------CAGCCCCCACCGCCTGCTGTGGCATGTGCAGCAGCAGCA 907
Db         99 ThrGluGlnProProSerProGlnProGlyProProAlaAlaSerHisThr-ProGluLy 118

Qy        906 GCAGGGGCTTTAGCTA----------------------------CATTCTCACACTAT 877
Db        118 sGlnAlaSerSerPheAspPheAsnGlyProTyrLeuGlyProProHisSerArgSer-L 138

Qy        876 TGAACACAGTGATGGGGCTGCCCACGGAACCGTCCCAGGGAGGGGCACAG------CCCC 823
Db        138 euProAspIleLeuGlyGlnProGluProProGlnGluGlyGlySerGlnLysSerProP 158

Qy        822 CAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCACAGGGTTGGAGAGGCAGTCATACC 763
Db        158 roProGlySerLeuGluTyrLeuCysLeu---ProAlaGlyGlyGlnValGlnLeuValP 177

Qy        762 CCCATGATTCCTGGACTAGGAGCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTT 703
```

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Db        177 ro---------------------------------------------------------- 177

Qy        702 AACATTTGGCATTATTGCACGTTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTT 643
Db        178 ----------------------------------------------------LeuAlaG 180

Qy        642 TGTCTGCAGGGGTTCCCAGGTGACATGCAGTGCTGCCAGTGCAAGTCACTCCCTCCACAG 583
Db        180 lnAlaMetGlyProGlyGln---------AlaValGluValGluArgArgProSerGlnG 197

Qy        582 GCAAGCCCAGCTGCTGAGGATAGTCAGCTGGTCAGCCGAGCCCTCAGATAGGTCAGCCAG 523
Db        197 ly--------------------AlaAlaGlySerProSerLeuGluSerGlyGly---- 208

Qy        522 AGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGCTCCATCCAGTCTTGA 463
Db        209 -------------------------GlyProAlaProProAlaLeuGlyPro------- 217

Qy        462 AAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGAGGTAACAGGGCTGGATGTTTCTC 403
Db        218 -------------ArgValGlyGlyGlnAspGlnLysAspSerProValAlaIleProM 233

Qy        402 TTTCTGGAGGCAAGACCATTCTCCCTAATTTGACTGCCTTGAAGACACGTATACCTCTCT 343
Db        233 etSerSerGlyAspThrGluAspProGlyValAlaSerGlyTyrValSer-SerAlaAsp 252

Qy        342 CTCATCACCTCAGCACCCCCTCTGACTTCCGATGGGGGATCACTATCTATCAACCTC--- 286
Db        253 LeuVal--------------PheThrProAsnSerGlyAlaSerSerValSerLeuVal 267

Qy        285 --------------------CAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCT--- 250
Db        268 ProSerLeuGlyLeuProSerAspGlnThrProSerLeuCysProGlyLeuAlaSerGly 287

Qy        249 CCCACTGGCTCACCTGTCCAGGTG--------------------GTCTGGTTGGTGACC 211
Db        288 ProProGlyAlaProGlyProValLysSerGlyPheGluGlyTyrValGluLeuProPro 307

Qy        210 ACAAAGGCCCGACACTGGGCATGGCTCTCACAGACATCCACAGCCT-------------- 165
Db        308 IleGluGlyArg-SerProArgSerProArgAsnAsnProValProProGluAlaLysSe 327

Qy        164 ----------CAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCGTGGTGGTAGGATGGC 115
Db        327 rProValLeuAsnProGly--------------------GluArgProAlaAspValSe 340

Qy        114 CAGCAGCGGTAGTCTTCCTGGGGGATGGTGCTGTCTGGGATACACTGGTACTCGGTACTG 55
Db        340 rProThrSerProGlnProGluGlyLeuLeuValLeuGlnGlnValGlyAsp---TyrCy 359

Qy         54 CTGCTTGCCG 45
Db        359 sPheLeuPro 362

RESULT 11
US-08-783-774-2
; Sequence 2, Application US/08783774
; Patent No. 6054130
;  GENERAL INFORMATION:
;    APPLICANT:  Spaete, Richard
;    APPLICANT:  Jackman, Winthrop
;    TITLE OF INVENTION:  NON-SPLICING VARIANTS OF
;    TITLE OF INVENTION:  GP350/220
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036/2711
;    COMPUTER READABLE FORM:
```

```
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/783,774
;       FILING DATE:  15-JAN-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Coruzzi, Laura A.
;       REGISTRATION NUMBER:  30,742
;       REFERENCE/DOCKET NUMBER:  7682-037
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-790-9090
;       TELEFAX:  212-869-8864
;       TELEX:  66141 PENNIE
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  907 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
US-08-783-774-2

Alignment Scores:
Pred. No.:                0.00538        Length:          907
Score:                    115.00         Matches:         90
Percent Similarity:       32.77%         Conservative:    46
Best Local Similarity:    21.69%         Mismatches:      117
Query Match:              4.49%          Indels:          162
DB:                       3              Gaps:            18

US-09-989-919-15 (1-1397) x US-08-783-774-2 (1-907)

Qy       1182 CCCACCCCCGCCCCAGGT---CCTGGCTCAAACCACACC---------------------- 1147
                 |||             |||   |||   |||   |||
Db        442 ProAsnThrThrThrGlyLeuProSerSerThrHisValProThrAsnLeuThrAlaPro 461

Qy       1146 TGCTCCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGG 1087
                 |||      |||   ::::::   |||:::|||      :::::::|||
Db        462 AlaSerThrGlyProThrValSerThrAlaAspVal------ThrSerPro--------- 476

Qy       1086 GCTGGCCTGGGAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCA 1027
                        :::|||   |||   :::       |||||||||   |||   |||
Db        477 --------------ThrProAlaGlyThrThrSerGlyAlaSerProValThrProSer 491

Qy       1026 CCCACATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACACT 967
                 |||:::   |||           :::         ||||||::::::         :::
Db        492 ProSerProTrpAspAsnGlyThrGluSerLysAlaProAspMetThrSerSerThrSer 511

Qy        966 CCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTGGCATGTGCAGCAGCAGCA 907
                 |||                |||   |||   |||   |||   :::         |||
Db        512 Pro------------ValThrThrProThrProAsnAlaThrSerProThrProAlaVal 527

Qy        906 GCAGGGGCTTTAGCTACATTCTCACACTATTGAACACAGTGATGGGGCTGCCCACGGAAC 847

Db        528 Thr---------------------------------------------------------- 528

Qy        846 CGTCCCAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCA 787
                                                                      :::|||
Db        529 ----------------------------------------------------ThrPro 530

Qy        786 CAGGGTTGGAGAGGCAGTCATACCCCCATGATT--------------------------- 754
                          |||   ||||||   :::
Db        531 ThrProAsnAlaThrSerProThrProAlaValThrThrProThrProAsnAlaThrSer 550

Qy        753 CCTGGACTAGGAGCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGG 694
                 |||   ||||||   :::||||||   :::   :::                |||
Db        551 ProThrLeuGlyLysThrSerProThrSerAlaValThrThrProThrProAsn------ 568

Qy        693 CATTATTGCACGTTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAG 634
                                      ||||||      ||||||    :::

Db        569 --------------------AlaThrSerProThrLeuGly-LysThr------SerPr 579

Qy        633 GGGTTCCCAGGTGACATGCAGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCAAG---- 578
                    |||   ||||||           :::|||::: :::|||:::   ||||||
Db        579 oThrSerAlaValThrThrProThrProAsnAlaThr-SerProThrLeuGlyLysThrS 599

Qy        577 ----------------------------CCCAGCTGCTGAGGATAGTCAGCTGGTCAGC 547
                                           |||:::      |||   :::   |||:::
Db        599 erProThrSerAlaValThrThrProThrProAsnAlaThrGlyProThrValGlyGluT 619

Qy        546 CGAGCCCTCAG------------------------------------------------- 536
                |||||||||
Db        619 hrSerProGlnAlaAsnAlaThrAsnHisThrLeuGlyGlyThrSerProThrProValV 639

Qy        535 --ATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGC 478
                  ||||||:::      |||      |||                ||||||
Db        639 alThrSerGlnProLysAsnAlaThrSerAlaVal--------------ThrThrGlyG 654

Qy        477 TCCATCCAGTCTTGAAAAAGACC-----------AGCTGCCGACCTGGGGGGCAGAGGT 430
                |||   :::         :::            |||   ||||||
Db        654 lnHisAsnIleThrSerSerSerThrSerSerMetSerLeuArgProSer---------- 670

Qy        429 GAGAGGTAACAGGGCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGA 370
                                                 |||      :::|||:::   |||:::   :
Db        671 ----------------------------SerAsnProGluThrLeuSerProSerThrS 681

Qy        369 CTGCCTTGAAGACACGTATACCTCTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGAT 310
                  ::         |||    ::::::   |||:::|||||||||   |||
Db        681 erAspAsnSerThrSer-HisMetProLeuLeuThrSerAlaHisPro---------Thr 697

Qy        309 GGGGGATCACTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCT 250
                |||||              |||:::    :::|||   |||:::   :::
Db        698 GlyGlyGlu---------AsnIle-ThrGlnValThrProAlaSerIle---------- 710

Qy        249 CCCACTGGCTCACCTGTCCAGGTGGTCTGGTTGGTGACCACAAAGGCCCGACACTGGGCA 190
                                                                   |||   ||
Db        711 ------------------------------------------------SerThrHisHi 714

Qy        189 TGGCTCTCACAGACATCCACAGCCTCAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCG 130
                |   |||         |||:::|||:::||||||   |||           :::
Db        714 sValSerThrSerSerProGluProArgProGlyThrThr---------SerGlnAlaSe 731

Qy        129 TGGTGGTAGGATGGCCAGCAGCGGTAGTCTTCCTGGG 93
                 |||          :::|||:::   :::   ||||||
Db        731 rGlyProGlyAsnSerSerThrSerThrLysProGly 743

RESULT 12
US-09-328-599A-1
; Sequence 1, Application US/09328599A
; Patent No. 6432679
;  GENERAL INFORMATION:
;    APPLICANT:  MOND, James J. and Lees, Andrew
;    TITLE OF INVENTION:  Enhancement of B Cell Activation by
;    TITLE OF INVENTION:  Co-Ligation of Receptors for Antigen and Complement C3d
;    TITLE OF INVENTION:  Using EBV gp350/220 or EBV gp350/220 Peptide Adjuvants
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner, L.L.P.
;      STREET:  1300 I Street, N.W., Suite 700
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/328,599A
;      FILING DATE:
;      CLASSIFICATION:
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  04995.6025-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)408-4000
;      TELEFAX:  (202)408-4400
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  907 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-328-599A-1

Alignment Scores:
Pred. No.:                0.00538        Length:          907
Score:                    115.00         Matches:         90
Percent Similarity:       32.77%         Conservative:    46
Best Local Similarity:    21.69%         Mismatches:      117
Query Match:              4.49%          Indels:          162
DB:                       4              Gaps:            18

US-09-989-919-15 (1-1397) x US-09-328-599A-1 (1-907)

Qy       1182 CCCACCCCCGCCCCAGGT---CCTGGCTCAAACCACACC---------------------- 1147
                 |||             |||  |||  |||  |||
Db        442 ProAsnThrThrThrGlyLeuProSerSerThrHisValProThrAsnLeuThrAlaPro 461

Qy       1146 TGCTCCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGG 1087
                 |||      |||  ::::::  |||:::|||     ::::::|||
Db        462 AlaSerThrGlyProThrValSerThrAlaAspVal------ThrSerPro--------- 476

Qy       1086 GCTGGCCTGGGAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCA 1027
                        :::|||  |||  :::     |||||||||  |||  |||
Db        477 --------------ThrProAlaGlyThrThrSerGlyAlaSerProValThrProSer 491

Qy       1026 CCCACATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACACT 967
                 |||:::  |||          :::         ||||||::::::          :::
Db        492 ProSerProTrpAspAsnGlyThrGluSerLysAlaProAspMetThrSerSerThrSer 511

Qy        966 CCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTGGCATGTGCAGCAGCAGCA 907
                 |||                 |||  |||  |||  |||  :::          |||
Db        512 Pro------------ValThrThrProThrProProAsnAlaThrSerProThrProAlaVal 527

Qy        906 GCAGGGGCTTTAGCTACATTCTCACACTATTGAACACAGTGATGGGGCTGCCCACGGAAC 847

Db        528 Thr---------------------------------------------------------- 528

Qy        846 CGTCCCAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCA 787
                                                                    :::|||
Db        529 ----------------------------------------------------ThrPro 530

Qy        786 CAGGGTTGGAGAGGCAGTCATACCCCCATGATT-------------------------- 754
                          |||   ||||||   :::
Db        531 ThrProAsnAlaThrSerProThrProAlaValThrThrProThrProAsnAlaThrSer 550

Qy        753 CCTGGACTAGGAGCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGG 694
                 |||   ||||||  :::||||||   :::  :::            |||
Db        551 ProThrLeuGlyLysThrSerProThrSerAlaValThrThrProThrProAsn------ 568

Qy        693 CATTATTGCACGTTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAG 634
                              ||||||      ||||||    :::
Db        569 ---------------------AlaThrSerProThrLeuGly-LysThr------SerPr 579

Qy        633 GGGTTCCCAGGTGACATGCAGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCAAG---- 578
                 |||   ||||||          :::|||::: :::|||:::   ||||||
Db        579 oThrSerAlaValThrThrProThrProAsnAlaThr-SerProThrLeuGlyLysThrS 599

Qy        577 ----------------------------CCCAGCTGCTGAGGATAGTCAGCTGGTCAGC 547
                                           |||:::      |||   :::   |||:::
Db        599 erProThrSerAlaValThrThrProThrProAsnAlaThrGlyProThrValGlyGluT 619

Qy        546 CGAGCCCTCAG------------------------------------------------- 536
                  |||||||||
Db        619 hrSerProGlnAlaAsnAlaThrAsnHisThrLeuGlyGlyThrSerProThrProValV 639

Qy        535 --ATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGC 478
                    ||||||:::      |||      |||                  ||||||
Db        639 alThrSerGlnProLysAsnAlaThrSerAlaVal--------------ThrThrGlyG 654

Qy        477 TCCATCCAGTCTTGAAAAAGACC------------AGCTGCCGACCTGGGGGGCAGAGGT 430
                  |||   :::          :::            |||   ||||||
Db        654 lnHisAsnIleThrSerSerSerThrSerSerMetSerLeuArgProSer---------- 670

Qy        429 GAGAGGTAACAGGGCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGA 370
                                              |||      :::|||:::   |||:::   :
Db        671 ----------------------------SerAsnProGluThrLeuSerProSerThrS 681

Qy        369 CTGCCTTGAAGACACGTATACCTCTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGAT 310
                 ::         |||    ::::::   |||:::|||||||||   |||
Db        681 erAspAsnSerThrSer-HisMetProLeuLeuThrSerAlaHisPro---------Thr 697

Qy        309 GGGGGATCACTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCT 250
                 ||||||              |||:::    :::|||   |||:::   :::
Db        698 GlyGlyGlu---------AsnIle-ThrGlnValThrProAlaSerIle---------- 710

Qy        249 CCCACTGGCTCACCTGTCCAGGTGGTCTGGTTGGTGACCACAAAGGCCCGACACTGGGCA 190
                                                                    |||   ||
Db        711 ----------------------------------------------------SerThrHisHi 714

Qy        189 TGGCTCTCACAGACATCCACAGCCTCAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCG 130
                 |   |||          |||:::|||:::||||||   |||                :::
Db        714 sValSerThrSerSerProGluProArgProGlyThrThr---------SerGlnAlaSe 731

Qy        129 TGGTGGTAGGATGGCCAGCAGCGGTAGTCTTCCTGGG 93
                  |||         :::|||:::   :::   ||||||
Db        731 rGlyProGlyAsnSerSerThrSerThrLysProGly 743

RESULT 13
PCT-US95-04611A-19
; Sequence 19, Application PC/TUS9504611A
;  GENERAL INFORMATION:
;    APPLICANT:  Spaete, Richard and Jackman, Winthrop, T.
;    TITLE OF INVENTION:  Non Splicing Variants of gp350/220
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooley Godward Castro Huddleson & Tatum
;      STREET:  5 Palo Alto Square
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94306
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patent In Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/04611A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/229,291
;      FILING DATE:  April 18, 1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Luann Cserr
;      REGISTRATION NUMBER:  31,822
;      REFERENCE/DOCKET NUMBER:  AVIR-003/00US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-5163
;      TELEFAX:  415-857-0663
;      TELEX:  380816 CooleyPA
;  INFORMATION FOR SEQ ID NO:  19:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  907 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-04611A-19

Alignment Scores:
Pred. No.:                0.00538        Length:          907
Score:                    115.00         Matches:         90
Percent Similarity:       32.77%         Conservative:    46
Best Local Similarity:    21.69%         Mismatches:      117
Query Match:              4.49%          Indels:          162
DB:                       5              Gaps:            18

US-09-989-919-15 (1-1397) x PCT-US95-04611A-19 (1-907)

Qy       1182 CCCACCCCCGCCCCAGGT---CCTGGCTCAAACCACACC---------------------- 1147
Db        442 ProAsnThrThrThrGlyLeuProSerSerThrHisValProThrAsnLeuThrAlaPro 461

Qy       1146 TGCTCCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGG 1087
Db        462 AlaSerThrGlyProThrValSerThrAlaAspVal------ThrSerPro--------- 476

Qy       1086 GCTGGCCTGGGAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCA 1027
Db        477 --------------ThrProAlaGlyThrThrSerGlyAlaSerProValThrProSer 491

Qy       1026 CCCACATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACACT 967
Db        492 ProSerProTrpAspAsnGlyThrGluSerLysAlaProAspMetThrSerSerThrSer 511

Qy        966 CCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTGGCATGTGCAGCAGCAGCA 907
Db        512 Pro------------ValThrThrProThrProAsnAlaThrSerProThrProAlaVal 527

Qy        906 GCAGGGGCTTTAGCTACATTCTCACACTATTGAACACAGTGATGGGGCTGCCCACGGAAC 847
Db        528 Thr---------------------------------------------------------- 528

Qy        846 CGTCCCAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCA 787
Db        529 ----------------------------------------------------------ThrPro 530

Qy        786 CAGGGTTGGAGAGGCAGTCATACCCCCATGATT--------------------------- 754
Db        531 ThrProAsnAlaThrSerProThrProAlaValThrThrProThrProAsnAlaThrSer 550

Qy        753 CCTGGACTAGGAGCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGG 694
Db        551 ProThrLeuGlyLysThrSerProThrSerAlaValThrThrProThrProAsn------ 568

Qy        693 CATTATTGCACGTTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAG 634
Db        569 --------------------AlaThrSerProThrLeuGly-LysThr------SerPr 579

Qy        633 GGGTTCCCAGGTGACATGCAGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCAAG---- 578
Db        579 oThrSerAlaValThrThrProThrProAsnAlaThr-SerProThrLeuGlyLysThrS 599

Qy        577 ----------------------------CCCAGCTGCTGAGGATAGTCAGCTGGTCAGC 547
Db        599 erProThrSerAlaValThrThrProThrProAsnAlaThrGlyProThrValGlyGluT 619

Qy        546 CGAGCCCTCAG------------------------------------------------- 536
Db        619 hrSerProGlnAlaAsnAlaThrAsnHisThrLeuGlyGlyThrSerProThrProValV 639

Qy        535 --ATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGC 478
Db        639 alThrSerGlnProLysAsnAlaThrSerAlaVal--------------ThrThrGlyG 654

Qy        477 TCCATCCAGTCTTGAAAAAGACC-----------AGCTGCCGACCTGGGGGGCAGAGGT 430
Db        654 lnHisAsnIleThrSerSerSerThrSerSerMetSerLeuArgProSer---------- 670

Qy        429 GAGAGGTAACAGGGCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGA 370
Db        671 ----------------------------SerAsnProGluThrLeuSerProSerThrS 681

Qy        369 CTGCCTTGAAGACACGTATACCTCTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGAT 310
Db        681 erAspAsnSerThrSer-HisMetProLeuLeuThrSerAlaHisPro---------Thr 697

Qy        309 GGGGGATCACTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCT 250
Db        698 GlyGlyGlu---------AsnIle-ThrGlnValThrProAlaSerIle---------- 710

Qy        249 CCCACTGGCTCACCTGTCCAGGTGGTCTGGTTGGTGACCACAAAGGCCCGACACTGGGCA 190
Db        711 ------------------------------------------------SerThrHisHi 714

Qy        189 TGGCTCTCACAGACATCCACAGCCTCAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCG 130
Db        714 sValSerThrSerSerProGluProArgProGlyThrThr---------SerGlnAlaSe 731

Qy        129 TGGTGGTAGGATGGCCAGCAGCGGTAGTCTTCCTGGG 93
Db        731 rGlyProGlyAsnSerSerThrSerThrLysProGly 743

RESULT 14
US-08-127-499A-8
; Sequence 8, Application US/08127499A
; Patent No. 5510264
;  GENERAL INFORMATION:
;    APPLICANT:  VAN ALSTYNE, Diane
;    APPLICANT:  SHARMA, Lawrence Rajendra
;    TITLE OF INVENTION:  ANTIBODIES WHICH BIND MENINGITIS RELATED
;    TITLE OF INVENTION:  HOMOLOGOUS ANTIGENIC SEQUENCES
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/127,499A
;      FILING DATE:  28-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  51916/102/INBI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1063 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-08-127-499A-8

Alignment Scores:
Pred. No.:                0.00577        Length:          1063
Score:                    115.00         Matches:         95
Percent Similarity:       31.65%         Conservative:    37
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Best Local Similarity:  22.78%          Mismatches:    136
Query Match:            4.49%           Indels:        149
DB:                     1               Gaps:          20

US-09-989-919-15 (1-1397) x US-08-127-499A-8 (1-1063)

Qy       1184 GCCCCACCCCCGCCCCAGGTCCTGGCTCAAACC---------ACACCTGCTCCCTGACCC 1134
Db         77 AlaProProProProGluGluArgGlnGluSerArgSerGlnThrProAlaProLysPro 96

Qy       1133 CAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGGGCTGGCCTGGGAG 1074
Db         97 SerArg-----------------AlaPro---ProGlnGlnProGln------------ 105

Qy       1073 TGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAG---------------AAT 1029
Db        106 -------------------------ProProArgMetGlnThrGlyArgGlyGlySer 116

Qy       1028 CACCCACATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGA--- 972
Db        117 AlaProArgProGluLeuGlyProProThrAsnProPheGlnAlaAlaValAlaArgGly 136

Qy        971 ---------ACACTCCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGT----- 926
Db        137 LeuArgProProLeuHisAspPro---AspThrGlu-AlaProThrGluAlaCysValTh 155

Qy        925 ----GGCATGTGCAGCAGCAGCAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACAC 870
Db        155 rSerTrpLeuTrpSerGluGlyGlnGlyAlaValPheTyrArgValAspLeuHisPheTh 175

Qy        869 AGTGATGGGGCTGCCCACGGAACCGTCCCAGGGA------------------------- 836
Db        175 rAsnLeuGlyThrProProLeuAspGluAspGlyArgTrpAspProAlaLeuMetTyrAs 195

Qy        835 -------GGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCACAGG 783
Db        195 nProCysGlyProGluProPro---AlaHisValValArgAlaTyrAsnGlnProAlaGl 214

Qy        782 GTTGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGAGCCAGCAGTCCCATAGCTA 723
Db        214 yAspValArgGlyValTrpGlyLysGlyGluArgThrTyrAlaGluGlnAspPheArgVa 234

Qy        722 GGCTGGTAAACTCACATTTTAACATTTGGCATTATTGCACGTTTGTCCTGGTCACATCTG 663
Db        234 lGlyGly------ThrArgTrpHisArgLeuLeu-----------------ArgMetPr 246

Qy        662 TCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGTGACATGCAGTGCTGCCAGT 603
Db        246 oValArgGlyLeuAspGlyAspSerAlaProLeuProPro---HisThrThrGluArgIl 265

Qy        602 GCAAGTCACTCCCTCCACAGGCAAGCCCAGCTGCTGAGGATAGTCAGCTGGTCAGCCG-- 545
Db        265 eGluThrArg-------------------------------SerAlaArgHisProTr 274

Qy        544 -AGCCCTCAGATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGAC 486
Db        274 pArgIleArgPheGlyAlaProGlnAlaPheLeuAlaGlyLeuLeuLeuAlaThrValAl 294

Qy        485 CACTTGGCTCCATCCAGTCTTGAAAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGA 426
Db        294 a-ValGlyThrAlaArgAlaGlyLeuGlnProArgAlaAspMet---------------- 308

Qy        425 GGTAACAGGGCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGACTGC 366
Db        308 ------------------------------------------------------------ 308

Qy        365 CTTGAAGACACGTATACCTCTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGATGGGG 306
Db        309 -------------------------------AlaAlaProProThr-LeuProGlnPro 317

Qy        305 GATCACTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCTCCCA 246
Db        318 ------------------------------------------------------Pro 318

Qy        245 CTGGCTCACCTGTCCAGGTGGTCTGGTTGGTGACCACAAAGGCCCGACACTGGGCATGGC 186
Db        319 CysAlaHisGlyGlnHisTyrGlyHisHisHisHisGlnLeuProPheLeuGlyHisAsp 338

Qy        185 TCTCACAGACATCCACAGCCTCAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCGTGGT 126
Db        339 GlyHisHis--------------------------------GlyGlyThrLeuArgVal 347

Qy        125 GGTAGGATGGCCAGCAGCGGTAGT--------------------CTTCCTGGGGGATGG 87
Db        348 GlyGlnHisTyrArgAsnAlaSerAspValLeuProGlyHisTrpLeuGlnGlyGlyTrp 367

Qy         86 TGCTGTCTGGGA------------TACACTGGTACTCGGTACTGC 54
Db        368 GlyCysTyrAsnLeuSerAspTrpHisGlnGlyThrHisValCys 382

RESULT 15
US-08-482-847-8
; Sequence 8, Application US/08482847
; Patent No. 5556757
;  GENERAL INFORMATION:
;    APPLICANT:  VAN ALSTYNE, Diane
;    APPLICANT:  SHARMA, Lawrence Rajendra
;    TITLE OF INVENTION:  PEPTIDES REPRESENTING EPITOPIC SITES FOR
;    TITLE OF INVENTION:  BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
;    TITLE OF INVENTION:  CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,847
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/127,499
;      FILING DATE:  28-SEP-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  51916/104/INBI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1063 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  unknown
US-08-482-847-8

Alignment Scores:
Pred. No.:              0.00577         Length:         1063
Score:                  115.00          Matches:        95
Percent Similarity:     31.65%          Conservative:   37
Best Local Similarity:  22.78%          Mismatches:     136
Query Match:            4.49%           Indels:         149
DB:                     1               Gaps:           20

US-09-989-919-15 (1-1397) x US-08-482-847-8 (1-1063)
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Qy       1184 GCCCCACCCCCGCCCCAGGTCCTGGCTCAAACC---------ACACCTGCTCCCTGACCC 1134
Db         77 AlaProProProProGluGluArgGlnGluSerArgSerGlnThrProAlaProLysPro 96

Qy       1133 CAGTCTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGGGCTGGCCTGGGAG 1074
Db         97 SerArg-----------------AlaPro---ProGlnGlnProGln------------ 105

Qy       1073 TGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAG---------------AAT 1029
Db        106 --------------------------ProProArgMetGlnThrGlyArgGlyGlySer 116

Qy       1028 CACCCACATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGA--- 972
Db        117 AlaProArgProGluLeuGlyProProThrAsnProPheGlnAlaAlaValAlaArgGly 136

Qy        971 ---------ACACTCCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGT----- 926
Db        137 LeuArgProProLeuHisAspPro---AspThrGlu-AlaProThrGluAlaCysValTh 155

Qy        925 ----GGCATGTGCAGCAGCAGCAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACAC 870
Db        155 rSerTrpLeuTrpSerGluGlyGlnGlyAlaValPheTyrArgValAspLeuHisPheTh 175

Qy        869 AGTGATGGGGCTGCCCACGGAACCGTCCCAGGGA-------------------------- 836
Db        175 rAsnLeuGlyThrProProLeuAspGluAspGlyArgTrpAspProAlaLeuMetTyrAs 195

Qy        835 -------GGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCTTGCTTACAGCCCACAGG 783
Db        195 nProCysGlyProGluProPro---AlaHisValValArgAlaTyrAsnGlnProAlaGl 214

Qy        782 GTTGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGAGCCAGCAGTCCCATAGCTA 723
Db        214 yAspValArgGlyValTrpGlyLysGlyGluArgThrTyrAlaGluGlnAspPheArgVa 234

Qy        722 GGCTGGTAAACTCACATTTTAACATTTGGCATTATTGCACGTTTGTCCTGGTCACATCTG 663
Db        234 lGlyGly------ThrArgTrpHisArgLeuLeu-----------------ArgMetPr 246

Qy        662 TCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGTGACATGCAGTGCTGCCAGT 603
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Qy        602 GCAAGTCACTCCCTCCACAGGCAAGCCCAGCTGCTGAGGATAGTCAGCTGGTCAGCCG-- 545
Db        265 eGluThrArg-------------------------------SerAlaArgHisProTr 274

Qy        544 -AGCCCTCAGATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGAC 486
Db        274 pArgIleArgPheGlyAlaProGlnAlaPheLeuAlaGlyLeuLeuLeuAlaThrValAl 294

Qy        485 CACTTGGCTCCATCCAGTCTTGAAAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGA 426
Db        294 a-ValGlyThrAlaArgAlaGlyLeuGlnProArgAlaAspMet---------------- 308

Qy        425 GGTAACAGGGCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTCCCTAATTTGACTGC 366
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Db        309 -------------------------------AlaAlaProProThr-LeuProGlnPro 317

Qy        305 GATCACTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCTCCCA 246
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Db        319 CysAlaHisGlyGlnHisTyrGlyHisHisHisHisGlnLeuProPheLeuGlyHisAsp 338

Qy        185 TCTCACAGACATCCACAGCCTCAGCCAGGTTGAACACTGAAAGGAGGCAGCTCCCGTGGT 126

Db        339 GlyHisHis-------------------------------GlyGlyThrLeuArgVal 347

Qy        125 GGTAGGATGGCCAGCAGCGGTAGT---------------------CTTCCTGGGGGATGG 87
Db        348 GlyGlnHisTyrArgAsnAlaSerAspValLeuProGlyHisTrpLeuGlnGlyGlyTrp 367

Qy         86 TGCTGTCTGGGA------------TACACTGGTACTCGGTACTGC 54
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Job time : 40.5 secs

GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: December 12, 2003, 18:33:56 ; Search time 47.5 Seconds
(without alignments)
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Perfect score: 2527
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Searched: 684280 seqs, 185983659 residues

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Listing first 45 summaries

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Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	283	11.1	52	10	US-09-989-919-83	Sequence 83, Appl
c 3	143	5.6	1426	15	US-10-322-579-15	Sequence 15, Appl
c 4	134.5	5.3	738	10	US-09-978-979-6	Sequence 6, Appli
c 5	134.5	5.3	738	15	US-10-057-487-6	Sequence 6, Appli
c 6	134	5.2	4123	15	US-10-213-509-5	Sequence 5, Appli
7	133.5	5.3	1150	12	US-10-140-472-531	Sequence 531, App
8	133.5	5.3	1150	12	US-10-141-761-531	Sequence 531, App
9	133.5	5.3	1150	12	US-10-142-885-531	Sequence 531, App
10	133.5	5.3	1150	12	US-10-158-790-531	Sequence 531, App
11	133.5	5.3	1150	12	US-10-137-871-531	Sequence 531, App
12	133.5	5.3	1150	12	US-10-140-805-531	Sequence 531, App
13	133.5	5.3	1150	12	US-10-140-864-531	Sequence 531, App
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15	133.5	5.3	1150	12	US-10-141-756-531	Sequence 531, App
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17	133.5	5.3	1150	15	US-10-123-155-531	Sequence 531, App
18	133.5	5.3	1150	16	US-10-146-731-531	Sequence 531, App
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21	130.5	5.2	1346	12	US-10-142-885-481	Sequence 481, App
22	130.5	5.2	1346	12	US-10-158-790-481	Sequence 481, App
23	130.5	5.2	1346	12	US-10-137-871-481	Sequence 481, App
24	130.5	5.2	1346	12	US-10-140-805-481	Sequence 481, App
25	130.5	5.2	1346	12	US-10-140-864-481	Sequence 481, App
26	130.5	5.2	1346	12	US-10-140-923-481	Sequence 481, App
27	130.5	5.2	1346	12	US-10-141-756-481	Sequence 481, App
28	130.5	5.2	1346	12	US-10-141-759-481	Sequence 481, App
29	130.5	5.2	1346	15	US-10-123-155-481	Sequence 481, App
30	130.5	5.2	1346	16	US-10-146-731-481	Sequence 481, App
31	124.5	4.9	1280	12	US-10-087-887-86	Sequence 86, Appl
c 32	122.5	4.8	647	14	US-10-086-464-2	Sequence 2, Appli
c 33	122.5	4.8	647	14	US-10-086-464-4	Sequence 4, Appli
c 34	122.5	4.8	721	14	US-10-086-464-5	Sequence 5, Appli
c 35	121.5	4.7	522	10	US-09-764-868-1138	Sequence 1138, Ap
c 36	121.5	4.7	524	10	US-09-764-868-761	Sequence 761, App
c 37	121.5	4.7	1386	12	US-10-327-414-2	Sequence 2, Appli
c 38	120.5	4.7	1236	12	US-10-116-275-207	Sequence 207, App
c 39	120.5	4.7	1236	15	US-10-176-847-68	Sequence 68, Appl
c 40	119.5	4.7	613	12	US-10-260-937-16	Sequence 16, Appl
c 41	118	4.6	897	14	US-10-099-895-1	Sequence 1, Appli
c 42	117	4.6	775	12	US-10-224-999A-3462	Sequence 3462, Ap
43	117	4.6	2447	12	US-10-140-472-291	Sequence 291, App
44	117	4.6	2447	12	US-10-141-761-291	Sequence 291, App
45	117	4.6	2447	12	US-10-142-885-291	Sequence 291, App

ALIGNMENTS

RESULT 1
US-09-989-919-84
; Sequence 84, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pr
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-989-919-84

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Db          1 ValLeuHisLeuTyrArgSerGlyGlnTyrLeuGlnAsnSerThrAlaSerSerSerThr 20

Qy         62 GAGTACCAGTGTATCCCAGACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCC 121
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Qy        122 TACCACCACGGGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGT 181
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Qy        182 GAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGAG 241
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Db         61 GluSerHisAlaGlnCysArgAlaPheValValThrAsnGlnThrThrTrpThrGlyGlu 80

Qy        242 CCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAGATAGT 301
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Qy        302 GATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGTGTCTT 361
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Qy        422 TACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGGAGCCA 481
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RESULT 2
US-09-989-919-83
; Sequence 83, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
;  APPLICANT: Macina, Roberto
;  APPLICANT:  Recipon, Herve
;  APPLICANT:  Pluta, Jason
;  APPLICANT:  Ghosh, Malavika
;  APPLICANT:  Sun, Yongming
;  APPLICANT:  Liu, Chenghua
;  TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro
;  FILE REFERENCE: DEX-0289
;  CURRENT APPLICATION NUMBER: US/09/989,919
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: 60/252,505
;  PRIOR FILING DATE: 2000-11-22
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
;   LENGTH: 52
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-989-919-83

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Qy        901 GGCTTTAGCTACATTCTCACACTATTGAACACAGTGATGGGGCTGCCCACGGAACCGTCC 842
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Db         21 GlyPheSerTyrIleLeuThrLeuLeuAsnThrValMetGlyLeuProThrGluProSer 40

Qy        841 CAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCC 806
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Db         41 GlnGlyGlyAlaGlnProProValGlyArgLeuAla 52

RESULT 3
US-10-322-579-15
; Sequence 15, Application US/10322579
; Publication No. US20030114413A1
; GENERAL INFORMATION:
;  APPLICANT: BASLER, Konrad
;  APPLICANT:  BRUNNER, Erich
;  APPLICANT:  FROESCH, Barbara
;  APPLICANT:  KRAMPS, Thomas
;  APPLICANT:  PETER, Oliver
;  TITLE OF INVENTION: ESSENTIAL DOWNSTREAM COMPONENT OF THE WINGLESS SIGNALING PATHWAY
;  TITLE OF INVENTION:  THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED THEREON
;  FILE REFERENCE: Q60361
;  CURRENT APPLICATION NUMBER: US/10/322,579
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/915,543
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,502
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 1426
;   TYPE: PRT
;   ORGANISM: Human lgs/bcl9
US-10-322-579-15

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Qy       1173 GCCCCAGGTCCTGGCTCA---------------------------------------- 1156
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Qy       1155 ---------AACCACACCTGCTCCCTGACCCCAGTCTTG--------------GCTCAT 1120
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Qy        795 TACAGCCCACAGGGTTGGAGAGGCAGTCATACCCCCATGATTCC------TGGACTAGGA 742
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Qy        741 GCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGGCATTATTGCACG 682
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Qy        681 TTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGT 622
Db        941 ----------------------------------LeuGlnSerProGlyIleProProA 949

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Qy        564 GATAGTCAGCTGGTCAGCCGAGCCCTCAGATAGGTCAGCCAGAGGCCTTCACATATGTGG 505
Db        967 -----SerGlyGlyProProProProThrAlaSerGlnProAlaSerValAsnIleProG 985

Qy        504 TCTTGTTGGGATCAGGGACCACTTGGCTCCATCCAGTCTTGAAAAAGACCAGCTGCCGAC 445
Db        985 lySerLeuProSerSerThrProTyrThrMetProProGluProThrLeuSerGlnAsnP 1005

Qy        444 CTGGGGGGCAGAGGTGAGAGGTAACAGGGCTGGATGTTTCTCTTTCTGGA---GGCAAGA 388
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Qy        387 CCATTCTCCCTAATTTGACTGCCTTGAAGACACGTATACCTCTCTCTCATCACCTCA--- 331
Db       1016 heAlaMetProSerSerThr-ProLeuTyrHisAspAlaIleLysThrValAlaSerSer 1035

Qy        330 ---------GCACCCCCTCTGACTTCCGATGGG--------------------GGATCA 301
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Qy        300 CTATCTATCAACCTCCAGAGAGGTCCTGCCATCTCC----------------------- 265
Db       1056 MetGlyIleAsnThrGln---AsnProArgIleSerGlyProAsnProValValProMet 1074

Qy        264 ---------------CTTGGAAGGGCTTCTCCCACTGGCTCACCTGTCCAGGTGG----- 225
Db       1075 ProThrLeuSerProMetGlyMetThrGln-ProLeuSerHisSerAsnGlnMetProSe 1094

Qy        224 ------------------------------------------------TCTGGTTGGTG 214
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Qy        125 ---------------GGTAGGATGGCCAGCAGCGGTAGTCTTCCTGGGGGATGGTGCTG 82
Db       1151 lProPheProHisAsnGlyProSerGlyGlyGlnGlySerPheProGlyGly-------- 1168

Qy         81 TCTGGGATACACTGGTACT-----------CGGTACTGCTGCTTGCCGTGGAGTTCTGC 34
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Qy         33 AGATACTGCC 24
Db       1188 aAspAlaAla 1191
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RESULT 4
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; Sequence 6, Application US/09978979
; Patent No. US20020151702A1
; GENERAL INFORMATION:
; APPLICANT: Racie, Lisa, A.
; Twine, Natalie, C.
; Agostino, Michael, J.
; Wolfman, Neil
; Morris, Elisabeth
; TITLE OF INVENTION: Aggrecanase Molecules
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/978,979
; FILING DATE: 16-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/241,469
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,345
; REFERENCE/DOCKET NUMBER: GI 5435p
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (973) 660-5000
; TELEFAX: (973) 683-4117
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-978-979-6

Alignment Scores:

Pred. No.:	0.00982	Length:	738
Score:	134.50	Matches:	136
Percent Similarity:	32.09%	Conservative:	45
Best Local Similarity:	24.11%	Mismatches:	170
Query Match:	5.25%	Indels:	214
DB:	10	Gaps:	29

US-09-989-919-15 (1-1397) x US-09-978-979-6 (1-738)

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Qy       1265 TTCAAACTCGAGGAAGGGGGAAAGCCTGGTTTTGGCTGCTTTGAGGCTTTCATTGAAAGC 1206
Db             2 PheGlyLeuGluHisAspGlyAlaProGlySerGlyCysGlyProSerGlyHisValMet  21

Qy       1205 AAATGAGGCAGAAAGGCCCCGGCCCCACCCCCGCCCCAGGTCCT-----------GGCT 1158
Db            22 AlaSerGluArgArgArgProAlaPro--AlaSerProGlyProProAlaAlaAlaGlyS  41

Qy       1157 CAAACCACACCTGCTCCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGC---------A 1107
Db            41 erCys***AlaCysSer---AspProSerLeuArgArgArgSerLeuCysTrpProProT  60

Qy       1106 CCTCTGCCCCTGACCCCTGGGCTGGC----------------------------CTGG 1077
Db            60 hrSerAlaPro---------AlaGlyAlaLeuValLeuValProAlaLysSerArgLeuL  77

Qy       1076 GAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCACCCACATCCT 1017
Db            77 euValGlyGlyAlaGlyArg---GluLeuLeuPheProLeuThrLysGlyHisAlaSerL  96

Qy       1016 GGAGCATC---CCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACACTCCACGAT 960
Db            96 ysArgPheHisProArgAlaHisSer------------------------------------ 104

Qy        959 GGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTG----------------------- 925
Db           105 -----------SerValProProProProGlyValHisProGlyThrGluProGlyLeuS 121

Qy        924 -----GCATGTGCAGCAGCAGCAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACAC 870
Db           121 erArgAlaLeuSerGlnArgMetThrGlyAlaLeuVal---------------------- 133

Qy        869 AGTGATGGGGCTGCCCACGG-----------------AACCGTCCCAGGGAGGGGCACA 828
Db           134 -----TrpAspProProArgProGlnProGlySerAlaGlyHisProArgAsnAlaHisL 152

Qy        827 GCCCCCAGTGGGGAGACTAGCCTGAG---------CTTGCTTACAGCCCACAGGGT---- 781
Db           152 euGlyLeuTyrTyrSerAlaAsnGluGlnCysArgValAlaPheGlyProLysAlaValA 172

Qy        780 --------TGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGA------------ 742
Db           172 laCysThrPheAlaArgGluHisLeuValSerLeuProAlaValAlaTrpAspTrpLeu* 192

Qy        741 --------GCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGGCATT 690
Db           192 **GlyProSerAlaSerProSerSerArgProProLys---------ArgAlaTrp-Ile 208

Qy        689 ATTGCACGTTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGT 630
Db           209 CysAlaArgProSerProAlaThrGlnThrArgTrp----------------------- 220

Qy        629 TCCCAGGTGACATGCAGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCAAGCCCAGCTG 570
Db           221 ---------ThrLysAlaAlaAlaAlaAlaSerSerPheLeuSerTrpMetGlyGlnAsn 237

Qy        569 CTG--------------------AGGATAGTCAGC------TGGTCAGCCGAGCCCTCA 537
Db           238 ValAlaTrpArgSerGlyAlaProArgValAlaAlaAlaProTrpTrpSer***ProPro 257

Qy        536 GATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGCT 477
Db           258 ***GlnGlnCysMetGly---------AlaGlyLeuAlaGlyValProGluValLeuAla 274

Qy        476 CCATCCAGTCTTGAAAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGAGGTAACAGG 417
Db           275 ProAlaProAlaGluGluValTrpSerPro-GlyGlyGly---------SerAlaThrTh 291

Qy        416 GCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTC---------------------- 380
Db           291 rProAspLeuProLeuGlyGlyValHisValLeuValLeuThrSerArgProArgCysAl 311

Qy        379 ----------------------------------------------------CCTAATTT 372
Db           311 aThrLeuArgProAlaArgArgProSerTrpSerSerCysArgAsnSerAlaProGlyPr 331

Qy        371 GACTGCCTTGAAGACACGTATACCTCTCTCT---------------------------- 341
Db           331 oThrAlaSerArgCysAlaProProLeuAlaAlaProProSerThrThrGlyValLeuLe 351

Qy        340 ----CATCACCTCAGCACCCCCTCTGACTTCCGAT------------------------ 310
Db           351 uTyrHis-ThrAlaLysGlyMetLeuCysAlaAspThrCysAlaGlyProLeuAlaArgA 371

Qy        309 -----GGGGGATCACTATCTATCAACCTCCAGAGAGGTCCTGCC---------ATCTCCC 264
Db           371 laSerSer***SerValGluThrAlaSerSerMetGlyProGlyValCysGlnValAlaP 391

Qy        263 TTGGAAGGGCTTCTCCC----------------------ACTGGCTCACCTGTCCAGG 228
Db           391 roGlyArgThrGlyPro***AlaCysValCysArgAlaAlaAlaGly-HisLeuAlaVal 410

Qy        227 TGGTCTGGTTGGTGACCACAAAGGCCCGACACTGGG----------------------- 192
Db           411 MetValGlyTrpThrProSerArgTyrGlyThrGlyAlaArgCysValValGlyThrThr 430

Qy        191 ------------CATGGCTCT---------------------------------------- 183
Db           431 AlaArgAlaAlaHisGlyArgAlaLeuSerGlnLeuAlaGluArgGluAsnMetSerArg 450

Qy        182 ---CACAGACATCCACAGCCTCAGCCAGGTTGAACACTG------AAAGGAGGCAGCTCC 132
Db           451 Phe***GlnLeuProProThr***ProValSerThrLeuProThrThrGlyLeuSerSer 470

Qy        131 CGTGGTGGTAGGATGGCCAGCAGCGGTAGTCT---------------------------- 100
Db           471 HisThrTrpArg***GlySerGluGlyAlaMetSerTrpLeuGlyArg***AlaSerPro 490

Qy         99 --------------------TCCTGGGGGATGGTGCTGTCTGGGATACACTGGTACTCG 61
Db           491 LeuThrProProThrProProSerTrpArgMetValValSerSerThrGluTrpProSer 510
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RESULT 5
US-10-057-487-6
; Sequence 6, Application US/10057487
; Publication No. US20030105313A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Aggrecanase Molecules
; FILE REFERENCE: 08702.0073
; CURRENT APPLICATION NUMBER: US/10/057,487
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/241,469
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 738
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (43)..(43)
; OTHER INFORMATION: unknown amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (192)..(192)
; OTHER INFORMATION: unknown amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (255)..(255)
; OTHER INFORMATION: unknown amino acid
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (258)..(258)

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;   OTHER INFORMATION: unknown amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (374)..(374)
;   OTHER INFORMATION: unknown amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (397)..(397)
;   OTHER INFORMATION: unknown amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (452)..(452)
;   OTHER INFORMATION: unknown amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (458)..(458)
;   OTHER INFORMATION: unknown amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (475)..(475)
;   OTHER INFORMATION: unknown amino acid
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (487)..(487)
;   OTHER INFORMATION: unknown amino acid
US-10-057-487-6

Alignment Scores:
Pred. No.:                0.00982        Length:          738
Score:                    134.50         Matches:         136
Percent Similarity:       32.09%         Conservative:    45
* Best Local Similarity:  24.11%         Mismatches:      170
- Query Match:            5.25%          Indels:          214
DB:                       15             Gaps:            29

US-09-989-919-15 (1-1397) x US-10-057-487-6 (1-738)

Qy       1265 TTCAAACTCGAGGAAGGGGGAAAGCCTGGTTTTGGCTGCTTTGAGGCTTTCATTGAAAGC 1206
                ||| |||||      ||| ||||||  ||||||      :::
Db          2 PheGlyLeuGluHisAspGlyAlaProGlySerGlyCysGlyProSerGlyHisValMet 21

Qy       1205 AAATGAGGCAGAAAGGCCCCGGCCCCACCCCCGCCCCAGGTCCT-----------GGCT 1158
                   |||:::  |||||||||     :::|||||||||          ||||
Db         22 AlaSerGluArgArgArgProAlaPro--AlaSerProGlyProProAlaAlaAlaGlyS 41

Qy       1157 CAAACCACACCTGCTCCCTGACCCCAGTCTTGGCTCATGCTGAGGTGTGC---------A 1107
                ||        ||||||      |||  |||           :::|||         |
Db         41 erCys***AlaCysSer---AspProSerLeuArgArgArgSerLeuCysTrpProProT 60

Qy       1106 CCTCTGCCCCTGACCCCTGGGCTGGC----------------------------CTGG 1077
                ||||||||||        ||||||                          |||
Db         60 hrSerAlaPro---------AlaGlyAlaLeuValLeuValProAlaLysSerArgLeuL 77

Qy       1076 GAGTGTCCCCTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCACCCACATCCT 1017
                  |||        ||||||  |||:::     |||  |||:::        |||
Db         77 euValGlyGlyAlaGlyArg---GluLeuLeuProLeuThrLysGlyHisAlaSerL 96

Qy       1016 GGAGCATC---CCCCGCCAAGTCTCCTGTCCAGACCTAAGCTGAGAGAACACTCCACGAT 960
                  ||||||      |||
Db         96 ysArgPheHisProArgAlaHisSer---------------------------------- 104

Qy        959 GGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTG---------------------- 925
                  :::  ||||||||||||  |||
Db        105 ----------SerValProProProProGlyValHisProGlyThrGluProGlyLeuS 121

Qy        924 -----GCATGTGCAGCAGCAGCAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACAC 870
                  |||  :::           |||||||||
Db        121 erArgAlaLeuSerGlnArgMetThrGlyAlaLeuVal--------------------- 133

Qy        869 AGTGATGGGGCTGCCCACGG-----------------AACCGTCCCAGGGAGGGGCACA 828
                  |||      ||||||                      ||||||      |||
Db        134 -----TrpAspProProArgProGlnProGlySerAlaGlyHisProArgAsnAlaHisL 152

Qy        827 GCCCCCAGTGGGGAGACTAGCCTGAG---------CTTGCTTACAGCCCACAGGGT---- 781
                     :::          |||         :::|||:::   |||:::
Db        152 euGlyLeuTyrTyrSerAlaAsnGluGlnCysArgValAlaPheGlyProLysAlaValA 172

Qy        780 --------TGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGA------------- 742
                     :::         |||         :::|||   :::
Db        172 laCysThrPheAlaArgGluHisLeuValSerLeuProAlaValAlaTrpAspTrpLeu* 192

Qy        741 --------GCCAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGGCATT 690
                     ::::::||||||   :::|||                          ||| |||
Db        192 **GlyProSerAlaSerProSerSerArgProProLys---------ArgAlaTrp-Ile 208

Qy        689 ATTGCACGTTTGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGT 630
                  ||||||   |||   :::      :::   |||
Db        209 CysAlaArgProSerProAlaThrGlnThrArgTrp----------------------- 220

Qy        629 TCCCAGGTGACATGCAGTGCTGCCAGTGCAAGTCACTCCCTCCACAGGCAAGCCCAGCTG 570
                     |||   :::||||||:::||||||      |||           |||
Db        221 ---------ThrLysAlaAlaAlaAlaAlaSerSerPheLeuSerTrpMetGlyGlnAsn 237

Qy        569 CTG--------------------AGGATAGTCAGC------TGGTCAGCCGAGCCCTCA 537
                  :::                |||:::   :::      |||   :::   |||
Db        238 ValAlaTrpArgSerGlyAlaProArgValAlaAlaAlaProTrpTrpSer***ProPro 257

Qy        536 GATAGGTCAGCCAGAGGCCTTCACATATGTGGTCTTGTTGGGATCAGGGACCACTTGGCT 477
                  :::          |||            ||||||   |||:::   :::   ||||||
Db        258 ***GlnGlnCysMetGly---------AlaGlyLeuAlaGlyValProGluValLeuAla 274

Qy        476 CCATCCAGTCTTGAAAAAGACCAGCTGCCGACCTGGGGGGCAGAGGTGAGAGGTAACAGG 417
                  |||:::      |||:::          |||    ||||||                |||
Db        275 ProAlaProAlaGluGluValTrpSerPro-GlyGlyGly---------SerAlaThrTh 291

Qy        416 GCTGGATGTTTCTCTTTCTGGAGGCAAGACCATTCTC---------------------- 380
                     |||:::   |||   |||        ::::::
Db        291 rProAspLeuProLeuGlyGlyValHisValLeuValLeuThrSerArgProArgCysAl 311

Qy        379 ----------------------------------------------------CCTAATTT 372
                                                                   |||
Db        311 aThrLeuArgProAlaArgArgProSerTrpSerSerCysArgAsnSerAlaProGlyPr 331

Qy        371 GACTGCCTTGAAGACACGTATACCTCTCTCT--------------------------- 341
                  ||||||   :::         ||||||:::
Db        331 oThrAlaSerArgCysAlaProProLeuAlaAlaProProSerThrThrGlyValLeuLe 351

Qy        340 ----CATCACCTCAGCACCCCCTCTGACTTCCGAT------------------------ 310
                     ||| |||:::         |||   :::|||
Db        351 uTyrHis-ThrAlaLysGlyMetLeuCysAlaAspThrCysAlaGlyProLeuAlaArgA 371

Qy        309 -----GGGGGATCACTATCTATCAACCTCCAGAGAGGTCCTGCC---------ATCTCCC 264
                        |||:::                |||||              :::::
Db        371 laSerSer***SerValGluThrAlaSerSerMetGlyProGlyValCysGlnValAlaP 391

Qy        263 TTGGAAGGGCTTCTCCC----------------------ACTGGCTCACCTGTCCAGG 228
                  ||||||   |||                     |||  ||||||:::
Db        391 roGlyArgThrGlyPro***AlaCysValCysArgAlaAlaAlaGly-HisLeuAlaVal 410

Qy        227 TGGTCTGGTTGGTGACCACAAAGGCCCGACACTGGG---------------------- 192
                     ||||||   |||   |||      ||||||
Db        411 MetValGlyTrpThrProSerArgTyrGlyThrGlyAlaArgCysValValGlyThrThr 430

Qy        191 ------------CATGGCTCT-----------------------------*--------- 183
                        ||||||
Db        431 AlaArgAlaAlaHisGlyArgAlaLeuSerGlnLeuAlaGluArgGluAsnMetSerArg 450

Qy        182 ---CACAGACATCCACAGCCTCAGCCAGGTTGAACACTG------AAAGGAGGCAGCTCC 132
                     :::  |||      |||      ||||||        |||   ||||||
Db        451 Phe***GlnLeuProProThr***ProValSerThrLeuProThrThrGlyLeuSerSer 470

Qy        131 CGTGGTGGTAGGATGGCCAGCAGCGGTAGTCT--------------------------- 100
                     |||      |||   |||:::
Db        471 HisThrTrpArg***GlySerGluGlyAlaMetSerTrpLeuGlyArg***AlaSerPro 490

Qy         99 --------------------TCCTGGGGGATGGTGCTGTCTGGGATACACTGGTACTCG 61
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Db        491 LeuThrProProThrProProSerTrpArgMetValValSerSerThrGluTrpProSer 510

RESULT 6
US-10-213-509-5
; Sequence 5, Application US/10213509
; Publication No. US20030054485A1
; GENERAL INFORMATION:
;  APPLICANT: Weiss, Joseph
;  APPLICANT:  Scott, Matthew
;  TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
;  FILE REFERENCE: STAN-232
;  CURRENT APPLICATION NUMBER: US/10/213,509
;  CURRENT FILING DATE:  2002-08-06
;  PRIOR APPLICATION NUMBER: 60/311,720
;  PRIOR FILING DATE: 2001-08-09
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4123
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-10-213-509-5

Alignment Scores:
Pred. No.:                0.0167          Length:          4123
Score:                    134.00          Matches:         110
Percent Similarity:       33.41%          Conservative:    36
Best Local Similarity:    25.17%          Mismatches:      134
Query Match:              5.23%           Indels:          157
DB:                       15              Gaps:            26

US-09-989-919-15 (1-1397) x US-10-213-509-5 (1-4123)

Qy       1249 GGGGAAAGCCTGGTTTTGGCTGCTTTGAGGCTTTCATTGAAAGCAAATGAGGCAGAAAGG 1190
              ||||||:::|||         :::|||   |||||||||              :::|||
Db       1799 GlyGluAlaLeuProSerGlySerLeuValLeuSerLeu--------------AspArg 1813

Qy       1189 CCCCGGCCCCACCCCCGCCCCAGGTCCTGGCTCAAACCACACCTGCTCCCTGACCCCAGT 1130
              |||      ||||||   |||   ||| ||||||:::         ||||||:::   ::
Db       1814 ProAlaAlaHisProProProProSer-GlySerAspCysTrpProSerLeuSerGlyLe 1833

Qy       1129 CTTGGCTCATGCTGAGGTGTGCACCTCTGCCCCTGACCCCTGGGCTGGCCTGG------G 1076
              : ||||||:::|||         |||         ||||||      |||       |
Db       1833 u-TrpLeuValLeu---LeuValThrLeuGlyGlnValProGlyProLeuTrpLysProG 1852

Qy       1075 AGTGTCCC------CTGTCGGGAGGTCAGAGATAGCCTCCCCAGGTACAGAATCACCCAC 1022
              ||   |||      |||      |||:::   ||||||                 |||
Db       1852 luHisProValValLeuProGluLeuGlnGlnProProProLeuArgProArgSerProV 1872

Qy       1021 ATCCTGGAGCATCCCCCGCCAAGTCTCCTGTCCAGACCT------------------AAG 980
                |||    |||||||||           :::   |||                  :::
Db       1872 alProTrp-HisProProGlnGlyThrGlnThrGluProCysGluGlyCysGluHisGln 1891

Qy        979 CTGAGAGAACACTCCACGATGGATTGTCCCCACGCAGCCCCCACCGCCTGCTGTGGCATG 920
                :::   |||        :::      |||      |||         |||   :::
Db       1892 GlyGlnValHisArgValGlyGluArgTrpHisGlyGlyPro---------CysArgVal 1908

Qy        919 TGCAGCAGCAGCAGCAGGGGCTTTAGCTACATTCTCACACTATTGAACACAGTGATGGGG 860
              |||                  |||      |||  |||
Db       1909 CysGln-CysLeuHisAsnLeuThrAlaHisCysSerProTyr---------------- 1922

Qy        859 CTGCCCACGGAACCGTCCCAGGGAGGGGCACAGCCCCCAGTGGGGAGACTAGCCTGAGCT 800
              ||||||                                                  ||
Db       1923 -CysPro-------------------------------------------------Le 1925

Qy        799 TGCTTACAGCCCACAGGGTTGGAGAGGCAGTCATACCCCCATGATTCCTGGACTAGGAGC 740
              |          ||||||||||||                  ::::::   |||   |||
Db       1925 uGlySerCysProGlnGlyTrp---------------ValLeuValGluGlyThrGlyGl 1940

Qy        739 CAGCAGTCCCATAGCTAGGCTGGTAAACTCACATTTTAACATTTGGCATTATTGCACGTT 680
              |||
Db       1940 uSer------------------------------------------------------- 1941

Qy        679 TGTCCTGGTCACATCTGTCTGTCTGGGATGTTAGCTTTGTCTGCAGGGGTTCCCAGGTGA 620
                                  |||      |||                  ||||||::
Db       1942 -------------------CysCysHisCys--------------AlaLeuProGlyGl 1950

Qy        619 CATGCAGTGCTGCCAGTGCAAGTCACTCCCT---------CCACAGGCAAGCCCAGCTGC 569
              :   |||       |||      :::   |||         |||       ||||||    :
Db       1950 uAsnGlnThrValGlnProMetAlaThrProAlaAlaAlaProAlaProSerProGln-I 1970

Qy        568 TGAGG------ATAGTCAGCTGGTCAGCCGAGCCCTCAGATAGGTCAGCCAGAGGCCTTC 515
              ::|||      :::   ::::::         ||||||      |||   |||   |||
Db       1970 leArgPheProLeuAlaThrTyrIleLeuProProSerGlyGlySerCysArgProLeuS 1990

Qy        514 AC------------ATATGT-------------------------------------G 506
                             |||                                       |
Db       1990 erSerProThrProAlaCysLeuSerLeuLeuHisProAspProCysTyrSerProLeuG 2010

Qy        505 GTCTTGTTGGGATCAGGGAC---------CACTTGGCTCCATCCAGTCTTGAAAAAGACC 455
              |||||   ||:::   :::          |||   :::          ||||||
Db       2010 lyLeuAlaGlyLeuAlaGluGlySerLeuHisAlaSerSerGlnGlnLeuGluHisProT 2030

Qy        454 AG------------------CTGCCGACCTGGGGGGCAGAGGTGAGAGGTAACAGGGCTG 413
                                   ||||||   |||        :::|||        ||||
Db       2030 hrGlnAlaAlaLeuLeuGlyAlaProThrGlnGlyProSerProGlnGlyTrpHisAlaG 2050

Qy        412 GA------TGTTTCTCTTTCTGGAGG---CAAGACCATTCTCCCTAATTTGACTGCCTTG 362
              ||        ::::::   |||      :::   |||             |||   |||:
Db       2050 lyGlyAspAlaTyrAlaLysTrpHisThrArgProHisTyrLeuGlnLeuAspLeuLeuG 2070

Qy        361 AA-------------------------------------------GACACGTATACCT 347
              ::                                           :::   |||   |
Db       2070 lnProArgAsnLeuThrGlyIleLeuValProGluThrGlySerSerAsnAlaTyrAlaS 2090

Qy        346 CTCTCTCATCACCTCAGCACCCCCTCTGACTTCCGATGGGGGATCACTATCTATCAACCT 287
              ||      |||  |||                  |||   |||:::
Db       2090 erSerPheSerLeuGlnPheSer---------SerAsnGlyLeuHisTrp---HisAspT 2106

Qy        286 CCAGAGAGGTCCTGCCATCTCCCTTGGAAGGGCTTCTCCCACTGGCTCACCTGTCC---- 231
                |||:::::::||||||             |||:::|||||||||      :::|||
Db       2106 yrArgAspLeuLeuPro------------GlyIleLeuProLeuProLysValSerProA 2122

Qy        230 --------AGGTGGTCT---------------------------------GGTTGGTGAC 212
                      ||||||                                          |
Db       2122 laGlnGlyArgTrpGlyGlnGlnProThrMetProPheCysGlyPheHisSerLeuCysP 2142

Qy        211 CACAAAGGCCCGACACT---------GGGCATGGCTCTCAC 180
              |||||   |||   :::         |||||||||   |||
Db       2142 roGlnGlyProSerSerValProGluGlyHisGlyLeuHis 2155

RESULT 7
US-10-140-472-531
; Sequence 531, Application US/10140472
; Publication No. US20030138888A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
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;  FILE REFERENCE: P3330R1C168
;  CURRENT APPLICATION NUMBER: US/10/140,472
;  CURRENT FILING DATE:  2002-05-06
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
;   LENGTH: 1150
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-140-472-531

Alignment Scores:
Pred. No.:              0.0134          Length:         1150
Score:                  133.50          Matches:        80
Percent Similarity:     26.21%          Conservative:   12
Best Local Similarity:  22.79%          Mismatches:     79
Query Match:            5.28%           Indels:         180
DB:                     12              Gaps:           13

US-09-989-919-15 (1-1397) x US-10-140-472-531 (1-1150)

Qy          3 TGCTGCACCTGT----------------------------------------ACCGGA 20
              ||||||||||||                                        |||
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
              |||   :::   |||   |||                   :::   :::   :::
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923

Qy         81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
                 |||   :::         |||   ||||||        ||||||||||||||||
Db        924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy        141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
              :::     |||:::          ||||||                      |||||
Db        944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy        177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
              | |||   :::   |||   |||   |||         |||      ||||||   ||||
Db        963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy        237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
              ||              |||
Db        983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy        297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
                                  ||||||                          ||||
Db        991 -------------------------GlyGly----------------------ThrC 994

Qy        357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
              ||
Db        994 ys------------------------------------------------------- 994

Qy        417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476

Db        994 ------------------------------------------------------------ 994

Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
                                              |||   |||         |||
Db        995 ---------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                |||     |||:::     ::::::   |||                 ||||||
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                |||   ||||||         ||||||:::|||||||||      ||||||   |||
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                      ||||||      |||
Db       1041 ------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                                      |||      |||
Db       1047 --------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
              ||||||||||||                                  ||| |||
Db       1058 ThrGlyGlyCysThrGly-----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
                                          |||||||||      ||||||||||       |
Db       1066 -------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGCTGCGTGGGGACA 955
              ||   |||||||||   ||||||
Db       1077 lyThrGlyGlyCysThrGlyThr 1084

RESULT 8
US-10-141-761-531
; Sequence 531, Application US/10141761
; Publication No. US20030148432A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C198
;  CURRENT APPLICATION NUMBER: US/10/141,761
;  CURRENT FILING DATE:  2002-05-08
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
;   LENGTH: 1150
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-141-761-531

Alignment Scores:
Pred. No.:              0.0134          Length:         1150
Score:                  133.50          Matches:        80
Percent Similarity:     26.21%          Conservative:   12
Best Local Similarity:  22.79%          Mismatches:     79
Query Match:            5.28%           Indels:         180
DB:                     12              Gaps:           13

US-09-989-919-15 (1-1397) x US-10-141-761-531 (1-1150)

Qy          3 TGCTGCACCTGT----------------------------------------ACCGGA 20
              ||||||||||||                                        |||
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
              |||   :::   |||   |||                   :::   :::   :::
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923
```

```
Qy         81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
Db        924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy        141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
Db        944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy        177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
Db        963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy        237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
Db        983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy        297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
Db        991 -------------------------GlyGly----------------------ThrC 994

Qy        357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
Db        994 ys------------------------------------------------------- 994

Qy        417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476
Db        994 ------------------------------------------------------- 994

Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
Db        995 ---------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
Db       1041 ---------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758
Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
Db       1047 -------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
Db       1058 ThrGlyGlyCysThrGly----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
Db       1066 ------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGCTGCGTGGGGACA 955
Db       1077 lyThrGlyGlyCysThrGlyThr 1084
```

RESULT 9
US-10-142-885-531
; Sequence 531, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; CURRENT FILING DATE: 2002-05-10
; Prior Apploication removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-142-885-531

Alignment Scores:

Pred. No.:	0.0134	Length:	1150
Score:	133.50	Matches:	80
Percent Similarity:	26.21%	Conservative:	12
Best Local Similarity:	22.79%	Mismatches:	79
Query Match:	5.28%	Indels:	180
DB:	12	Gaps:	13

US-09-989-919-15 (1-1397) x US-10-142-885-531 (1-1150)

```
Qy          3 TGCTGCACCTGT-----------------------------------------ACCGGA 20
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923

Qy         81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
Db        924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy        141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
Db        944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy        177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
Db        963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy        237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
Db        983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy        297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
Db        991 -------------------------GlyGly----------------------ThrC 994

Qy        357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
Db        994 ys------------------------------------------------------- 994

Qy        417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476
Db        994 ------------------------------------------------------- 994

Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
```

```
                                          |||   |||         |||
Db        995 ----------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                 |||      |||:::     ::::::   |||              ||||||
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                |||   ||||||         ||||||:::|||||||||      ||||||   |||
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                    ||||||     |||
Db       1041 ------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                          |||      |||
Db       1047 --------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
                |||||||||||                                 ||| |||
Db       1058 ThrGlyGlyCysThrGly----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
                                    |||||||||      ||||||||||       |
Db       1066 ------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGCTGCGTGGGGACA 955
                ||   |||||||||   ||||||
Db       1077 lyThrGlyGlyCysThrGlyThr 1084

RESULT 10
US-10-158-790-531
; Sequence 531, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C448
;  CURRENT APPLICATION NUMBER: US/10/158,790
;  CURRENT FILING DATE:  2002-05-30
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
;   LENGTH: 1150
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-158-790-531

Alignment Scores:
Pred. No.:              0.0134        Length:        1150
Score:                  133.50        Matches:       80
Percent Similarity:     26.21%        Conservative:  12
Best Local Similarity:  22.79%        Mismatches:    79
Query Match:            5.28%         Indels:        180
DB:                     12            Gaps:          13

US-09-989-919-15 (1-1397) x US-10-158-790-531 (1-1150)

Qy          3 TGCTGCACCTGT-----------------------------------------ACCGGA 20
              ||||||||||||                                         |||
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
              |||   :::   |||   |||                        :::   :::   :::
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923

Qy         81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
                 |||   :::         |||   ||||||         ||||||||||||||||||
Db        924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy        141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
              :::      |||:::          ||||||                      |||||
Db        944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy        177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
              | |||   :::   |||   |||  |||          |||        ||||||  ||||
Db        963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy        237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
              ||          |||
Db        983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy        297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
                                          ||||||                  ||||
Db        991 -------------------------GlyGly----------------------ThrC 994

Qy        357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
              ||
Db        994 ys------------------------------------------------------- 994

Qy        417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476

Db        994 ------------------------------------------------------------ 994

Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
                                                  |||   |||         |||
Db        995 ----------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                 |||      |||:::     ::::::   |||              ||||||
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                |||   ||||||         ||||||:::|||||||||      ||||||   |||
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                    ||||||     |||
Db       1041 ------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                          |||      |||
Db       1047 --------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
                |||||||||||                                 ||| |||
Db       1058 ThrGlyGlyCysThrGly----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
                                    |||||||||      ||||||||||       |
```

```
Db       1066 -------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGCTGCGTGGGGACA 955
              ||   |||||||||   ||||||
Db       1077 lyThrGlyGlyCysThrGlyThr 1084
```

RESULT 11
US-10-137-871-531
; Sequence 531, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C153
; CURRENT APPLICATION NUMBER: US/10/137,871
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-871-531

Alignment Scores:

Pred. No.:	0.0134	Length:	1150
Score:	133.50	Matches:	80
Percent Similarity:	26.21%	Conservative:	12
Best Local Similarity:	22.79%	Mismatches:	79
Query Match:	5.28%	Indels:	180
DB:	12	Gaps:	13

US-09-989-919-15 (1-1397) x US-10-137-871-531 (1-1150)

```
Qy          3 TGCTGCACCTGT-----------------------------------------ACCGGA 20
              ||||||||||||                                         |||
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
              |||   :::   |||   |||                    :::   :::   :::
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923

Qy         81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
                |||   :::       |||   ||||||        ||||||||||||||||||
Db        924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy        141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
              :::     |||:::         ||||||                      |||||
Db        944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy        177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
              | |||   :::   |||   |||   |||         |||      ||||||   ||||
Db        963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy        237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
              ||               |||
```

```
Db        983 lyGlyCysAlaAlaGlyAlaCys----------------------------------- 990

Qy        297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
                                      ||||||                        ||||
Db        991 -------------------------GlyGly-----------------------ThrC 994

Qy        357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
              ||
Db        994 ys------------------------------------------------------- 994

Qy        417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476

Db        994 ------------------------------------------------------------ 994

Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
                                                  |||   |||         |||
Db        995 ---------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                |||      |||:::      ::::::   |||              ||||||
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                |||   ||||||         |||||:::||||||||||      ||||||   |||
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                  ||||||      |||
Db       1041 -------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                                |||      |||
Db       1047 -------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
              ||||||||||                                      ||| |||
Db       1058 ThrGlyGlyCysThrGly----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
                                    |||||||||      ||||||||||||      |
Db       1066 -------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGCTGCGTGGGGACA 955
              ||   |||||||||   ||||||
Db       1077 lyThrGlyGlyCysThrGlyThr 1084
```

RESULT 12
US-10-140-805-531
; Sequence 531, Application US/10140805
; Publication No. US20030207417A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

```
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C176
;  CURRENT APPLICATION NUMBER: US/10/140,805
;  CURRENT FILING DATE:  2002-05-07
;  Prior Apploication removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
;   LENGTH: 1150
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-140-805-531

Alignment Scores:
Pred. No.:                0.0134          Length:          1150
Score:                    133.50          Matches:         80
Percent Similarity:       26.21%          Conservative:    12
Best Local Similarity:    22.79%          Mismatches:      79
Query Match:              5.28%           Indels:          180
DB:                       12              Gaps:            13

US-09-989-919-15 (1-1397) x US-10-140-805-531 (1-1150)

Qy          3 TGCTGCACCTGT----------------------------------------ACCGGA 20
              ||||||||||||                                        |||
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
              |||   :::   |||   |||                 :::   :::   :::
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923

Qy         81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
                 |||   :::         |||   ||||||        ||||||||||||||||
Db        924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy        141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
              :::      |||:::          ||||||                      |||||
Db        944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy        177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
              | |||   :::   |||  |||   |||         |||      ||||||   ||||
Db        963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy        237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
              ||                  |||
Db        983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy        297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
                                  ||||||                        ||||
Db        991 -------------------------GlyGly----------------------ThrC 994

Qy        357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
              ||
Db        994 ys------------------------------------------------------- 994

Qy        417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476

Db        994 ------------------------------------------------------------ 994

Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
                                          |||   |||      |||
Db        995 ---------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                |||      |||:::      ::::::   |||               ||||||
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                |||   ||||||         ||||||:::|||||||||      ||||||   |||
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                  ||||||     |||
Db       1041 ---------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                                      |||      |||
Db       1047 --------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
                ||||||||||||                                    ||| |||
Db       1058 ThrGlyGlyCysThrGly-----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
                                      |||||||||      ||||||||||||       |
Db       1066 ------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGCTGCGTGGGGACA 955
              ||   |||||||||   ||||||
Db       1077 lyThrGlyGlyCysThrGlyThr 1084

RESULT 13
US-10-140-864-531
; Sequence 531, Application US/10140864
; Publication No. US20030207419A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C184
;  CURRENT APPLICATION NUMBER: US/10/140,864
;  CURRENT FILING DATE:  2002-05-07
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
;   LENGTH: 1150
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-140-864-531

Alignment Scores:
Pred. No.:                0.0134          Length:          1150
Score:                    133.50          Matches:         80
Percent Similarity:       26.21%          Conservative:    12
Best Local Similarity:    22.79%          Mismatches:      79
Query Match:              5.28%           Indels:          180
DB:                       12              Gaps:            13

US-09-989-919-15 (1-1397) x US-10-140-864-531 (1-1150)

Qy          3 TGCTGCACCTGT----------------------------------------ACCGGA 20
              ||||||||||||                                        |||
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
              |||   :::   |||   |||                 :::   :::   :::
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923
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Qy          81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
               |||   :::         |||   ||||||         ||||||||||||||||||
Db         924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy         141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
               :::      |||:::       ||||||                       |||||
Db         944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy         177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
               | |||   :::   |||   |||   |||         |||      ||||||   ||||
Db         963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy         237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
               ||                |||
Db         983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy         297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
                                     ||||||                       ||||
Db         991 ------------------------GlyGly----------------------ThrC 994

Qy         357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
               ||
Db         994 ys------------------------------------------------------- 994

Qy         417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476

Db         994 ------------------------------------------------------------ 994

Qy         477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
                                        |||   |||       |||
Db         995 ---------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy         537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                  |||      |||:::      ::::::   |||               ||||||
Db        1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy         588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                  |||   ||||||         ||||||:::|||||||||      ||||||   |||
Db        1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy         639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                 ||||||     |||
Db        1041 ---------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy         699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db        1046 ------------------------------------------------------------ 1046

Qy         759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                           |||      |||
Db        1047 --------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy         819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
               ||||||||||||                                  ||| |||
Db        1058 ThrGlyGlyCysThrGly----------------------------Thr-Cys----- 1065

Qy         879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
                                           |||||||||      ||||||||||       |
Db        1066 ------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy         933 GCGGTGGGGGCTGCGTGGGGACA 955
               ||   |||||||||  ||||||
Db        1077 lyThrGlyGlyCysThrGlyThr 1084

RESULT 14
US-10-140-923-531
; Sequence 531, Application US/10140923
; Publication No. US20030207355A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C188
;  CURRENT APPLICATION NUMBER: US/10/140,923
;  CURRENT FILING DATE:  2002-05-07
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
;   LENGTH: 1150
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-140-923-531

Alignment Scores:
Pred. No.:                0.0134          Length:          1150
Score:                    133.50          Matches:         80
Percent Similarity:       26.21%          Conservative:    12
Best Local Similarity:    22.79%          Mismatches:      79
Query Match:              5.28%           Indels:          180
DB:                       12              Gaps:            13

US-09-989-919-15 (1-1397) x US-10-140-923-531 (1-1150)

Qy           3 TGCTGCACCTGT-------------------------------------------ACCGGA 20
               ||||||||||||                                           |||
Db         884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy          21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
               |||   :::   |||   |||                    :::   :::   :::
Db         904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923

Qy          81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
                  |||   :::         |||   ||||||         ||||||||||||||||||
Db         924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy         141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT----------------------GGATG 176
               :::      |||:::       ||||||                       |||||
Db         944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy         177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
               | |||   :::   |||   |||   |||         |||      ||||||   ||||
Db         963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy         237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
               ||                |||
Db         983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy         297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
                                     ||||||                       ||||
Db         991 ------------------------GlyGly----------------------ThrC 994

Qy         357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
               ||
Db         994 ys------------------------------------------------------- 994

Qy         417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476

Db         994 ------------------------------------------------------------ 994
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```
Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
                                                 |||   |||         |||
Db        995 ---------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                  |||      |||:::      ::::::   |||               ||||||
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                 |||   ||||||         ||||||:::|||||||||      ||||||   |||
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                    ||||||      |||
Db       1041 ---------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                           |||      |||
Db       1047 --------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
                |||||||||||                                  ||| |||
Db       1058 ThrGlyGlyCysThrGly-----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
                                  |||||||||      ||||||||||||       |
Db       1066 ------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGGCTGCGTGGGGACA 955
                ||   |||||||||   ||||||
Db       1077 lyThrGlyGlyCysThrGlyThr 1084
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RESULT 15
US-10-141-756-531
; Sequence 531, Application US/10141756
; Publication No. US20030207359A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C200
; CURRENT APPLICATION NUMBER: US/10/141,756
; CURRENT FILING DATE: 2002-05-08
; Prior Apploication removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 531
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-756-531

Alignment Scores:
Pred. No.: 0.0134 Length: 1150

Score: 133.50 Matches: 80
Percent Similarity: 26.21% Conservative: 12
Best Local Similarity: 22.79% Mismatches: 79
Query Match: 5.28% Indels: 180
DB: 12 Gaps: 13

US-09-989-919-15 (1-1397) x US-10-141-756-531 (1-1150)

```
Qy          3 TGCTGCACCTGT-------------------------------------------ACCGGA 20
              ||||||||||||                                           |||
Db        884 CysCysThrCysCysCysThrGlyThrAlaAlaGlyThrCysThrAlaThrThrThrAla 903

Qy         21 GCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACCAGTGTATCCCAG 80
              |||   :::   |||   |||                          :::   :::   :::
Db        904 AlaAlaAlaAlaCysAlaThrCysGlyAlaCysGlyAlaThrAlaCysAlaThrThrGly 923

Qy         81 ACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGCC 140
                 |||   :::          |||   ||||||         ||||||||||||||||||
Db        924 AlaAlaAlaThrGlyThrGlyThrGlyAlaAlaCysGlyThrThrThrThrGlyAlaAla 943

Qy        141 TCCTTTCAGTGTTCAACCTGGCTGAGGCTGT-----------------------GGATG 176
              :::      |||:::          ||||||                       |||||
Db        944 AlaAlaGlyCysThrAlaCysAla-GlyCysThrThrCysCysAlaGlyCysAlaGlyCy 963

Qy        177 TCTGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAG 236
              | |||   :::   |||   |||   |||         |||      ||||||   ||||
Db        963 s-CysAlaAlaAlaAlaGlyCysAlaAlaCysThrGlyThrThrGlyThrThrThrThrG 983

Qy        237 GTGAGCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAG 296
              ||               |||
Db        983 lyGlyCysAlaAlaGlyAlaCys---------------------------------- 990

Qy        297 ATAGTGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGT 356
                                  ||||||                          ||||
Db        991 -------------------------GlyGly-----------------------ThrC 994

Qy        357 GTCTTCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGC 416
              ||
Db        994 ys------------------------------------------------------- 994

Qy        417 CCTGTTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGG 476

Db        994 ------------------------------------------------------------ 994

Qy        477 AGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATC 536
                                                 |||   |||         |||
Db        995 ---------------------------------CysThrGlyAlaThrGlyThrAlaC 1003

Qy        537 TGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGG---------CTTGCCTGTG 587
                  |||      |||:::      ::::::   |||               ||||||
Db       1003 ysAlaAlaGlyCysThrThrGlyAlaThrThrGlyAlaAlaAlaThrThrCysAlaCys- 1022

Qy        588 GAGGGAGTGACTTGC---------ACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCA 638
                 |||   ||||||         ||||||:::|||||||||      ||||||   |||
Db       1023 ThrGlyCysThrCysAlaCysThrThrGlyAlaThrAlaCys------GlyThrThrAla 1040

Qy        639 GACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAA 698
                                                    ||||||      |||
Db       1041 ---------------------------------------ThrThrCysAlaGlyAla--- 1046

Qy        699 TGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCA 758

Db       1046 ------------------------------------------------------------ 1046

Qy        759 TGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCC 818
                                           |||      |||
Db       1047 --------------------------AlaAlaCysCysCysAlaAlaGlyGlyAlaAla 1057

Qy        819 ACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAAT 878
                |||||||||||                                  ||| |||
Db       1058 ThrGlyGlyCysThrGly-----------------------------Thr-Cys----- 1065

Qy        879 AGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGC------TGCTGCACATGCCACAGCAG 932
```

```
                                    |||||||||      ||||||||||||       |
Db       1066 -------------------------CysCysCysAlaThrCysCysThrCys-AlaThrG 1077

Qy        933 GCGGTGGGGGCTGCGTGGGGACA 955
              ||   |||||||||   ||||||
Db       1077 lyThrGlyGlyCysThrGlyThr 1084
```

Search completed: December 12, 2003, 18:46:13
Job time : 72.5 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 18:11:58 ; Search time 80 Seconds
(without alignments)
7707.653 Million cell updates/sec

Title: US-09-989-919-15
Perfect score: 1397
Sequence: 1 ggtgctgcacctgtaccgga.....aaaaaaaaaaaaaggcggtc 1397

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	46	3.3	2773	4	US-09-996-243-178	Sequence 178, App
	2	44.6	3.2	1037	4	US-09-489-847-112	Sequence 112, App
	3	44.6	3.2	1342	4	US-09-489-847-89	Sequence 89, Appl
c	4	44	3.1	1037	4	US-09-489-847-112	Sequence 112, App
	5	43.2	3.1	2223	1	US-08-257-073-4	Sequence 4, Appli
	6	43	3.1	441	4	US-09-601-537-10	Sequence 10, Appl
	7	43	3.1	944	3	US-08-906-769-82	Sequence 82, Appl
	8	43	3.1	944	3	US-08-906-616-82	Sequence 82, Appl
	9	43	3.1	944	3	US-08-817-795-82	Sequence 82, Appl
	10	43	3.1	944	3	US-08-639-075A-82	Sequence 82, Appl
	11	43	3.1	944	3	US-09-012-431-82	Sequence 82, Appl
	12	43	3.1	944	3	US-09-012-692-82	Sequence 82, Appl
	13	43	3.1	944	3	US-08-906-613-82	Sequence 82, Appl
	14	43	3.1	944	5	PCT-US95-14442A-82	Sequence 82, Appl
	15	43	3.1	945	3	US-09-032-215-26	Sequence 26, Appl
c	16	43	3.1	945	3	US-09-032-215-28	Sequence 28, Appl
	17	43	3.1	1582	3	US-08-545-196B-10	Sequence 10, Appl
	18	43	3.1	1582	3	US-08-545-196B-12	Sequence 12, Appl
	19	43	3.1	4121	4	US-09-601-537-9	Sequence 9, Appli
	20	42.8	3.1	1052	4	US-09-489-847-23	Sequence 23, Appl
	21	42.6	3.0	1361	4	US-09-489-847-64	Sequence 64, Appl
	22	42.6	3.0	1492	4	US-09-369-247-23	Sequence 23, Appl
c	23	42.6	3.0	7218	1	US-08-232-463-14	Sequence 14, Appl
c	24	42	3.0	5852	1	US-07-867-106-2	Sequence 2, Appli
	25	41.8	3.0	4203	2	US-08-866-757-1	Sequence 1, Appli
	26	41.8	3.0	4203	3	US-09-153-593-1	Sequence 1, Appli
	27	41.4	3.0	731	4	US-09-288-143-38	Sequence 38, Appl
	28	41.4	3.0	2136	4	US-09-996-243-302	Sequence 302, App
	29	41.4	3.0	3715	4	US-09-234-245-1	Sequence 1, Appli
	30	41.4	3.0	6152	3	US-08-973-462-1	Sequence 1, Appli
c	31	41.4	3.0	37950	3	US-09-338-907-183	Sequence 183, App
c	32	41.4	3.0	37950	4	US-09-218-207-183	Sequence 183, App
	33	41.2	2.9	2434	4	US-09-489-847-67	Sequence 67, Appl
	34	40.8	2.9	198	1	US-08-330-108-16	Sequence 16, Appl
	35	40.8	2.9	198	5	PCT-US92-10087-16	Sequence 16, Appl
	36	40.8	2.9	949	4	US-09-489-847-35	Sequence 35, Appl
	37	40.4	2.9	144	1	US-08-702-344-26	Sequence 26, Appl
	38	40.4	2.9	1474	3	US-08-821-994-64	Sequence 64, Appl
c	39	40.4	2.9	3138	1	US-07-867-106-4	Sequence 4, Appli
	40	40	2.9	1683	3	US-09-347-803-11	Sequence 11, Appl
	41	40	2.9	2447	2	US-09-014-969-14	Sequence 14, Appl
	42	39.8	2.8	1129	4	US-09-227-357-40	Sequence 40, Appl
	43	39.8	2.8	3989	4	US-09-205-258-28	Sequence 28, Appl
	44	39.6	2.8	1114	4	US-09-152-060-41	Sequence 41, Appl
	45	39.6	2.8	2013	4	US-09-596-196-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-996-243-178
; Sequence 178, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C13
; CURRENT APPLICATION NUMBER: US/09/996,243
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-09
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; PRIOR FILING DATE: 1998-06-10
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/090246
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02

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;  PRIOR APPLICATION NUMBER: 60/091978
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

  Query Match             3.3%;  Score 46;  DB 4;  Length 2773;
  Best Local Similarity   57.7%;  Pred. No. 0.011;
  Matches   82;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy       1249 CCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATT 1308
              || ||  | ||||| | | |     |      ||||    ||| ||  | || ||||||
Db       2584 CCCTCAGCAAGTTTCATTTTTGTCATGACAATGTAGGAATTGCTGAATTAAATGTTTAGA 2643

Qy       1309 TTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCT 1368
                | |||||||||| |||| |   || ||||  |       | |  |||
Db       2644 AGGATGAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2703

Qy       1369 AAAAAAAAAAAAAAAAAAAAA 1390
              |||||||||||||||||||||
Db       2704 AAAAAAAAAAAAAAAAAAAAA 2725


RESULT 2
US-09-489-847-112
; Sequence 112, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
;    LENGTH: 1037
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (936)
;    OTHER INFORMATION: n equals a,t,g, or c
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (946)
;    OTHER INFORMATION: n equals a,t,g, or c
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (951)
;    OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-112

  Query Match             3.2%;  Score 44.6;  DB 4;  Length 1037;
  Best Local Similarity   61.8%;  Pred. No. 0.015;
  Matches   68;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy       1281 GTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAA 1340
              | | || || ||      ||| |||| ||||  |||||| |||| ||||  |   || ||
Db        920 GGATTTTTTTTTTAAANGATTTTTTANTTTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAA 979

Qy       1341 AATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAAAAAAAAAAA 1390
              ||  |      | |  |||          |||||||||||||||||||||
Db        980 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1029


RESULT 3
US-09-489-847-89
; Sequence 89, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
;    LENGTH: 1342
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-489-847-89

  Query Match             3.2%;  Score 44.6;  DB 4;  Length 1342;
  Best Local Similarity   58.8%;  Pred. No. 0.018;
  Matches   77;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
              | | ||| |  ||||| |||| ||  |||  |  | ||| |  ||        ||||||
Db       1208 TGTAAATGTTAAGAATTTTTTTTATATCTGTTAAATAAAAATTATTTCCAAAAAAAAAAA 1267

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
                |||| ||||  |   || ||||  |      | |  |||           ||||||||||
Db       1268 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1327

Qy       1380 AAAAAAAAAAA 1390
              ||||||||||
Db       1328 AAAAAAAAAAA 1338


RESULT 4
US-09-489-847-112/c
; Sequence 112, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
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;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
;   LENGTH: 1037
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (936)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (946)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (951)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-489-847-112

  Query Match             3.1%;  Score 44;  DB 4;  Length 1037;
  Best Local Similarity   63.1%;  Pred. No. 0.022;
  Matches   65;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy       1275 TCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGT 1334
             | |||| |  || || ||  ||   || ||| ||||| | |||| ||||| |   ||
Db        990 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTNAAAANTAAAAAATCNTTTAA 931

Qy       1335 TAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAA 1377
              || |||||     | | |  |||||||| ||| ||| ||| |
Db        930 AAAAAAAATCCCCCTCCCCTCCAAACTCTCCCCAAAATAAATA 888


RESULT 5
US-08-257-073-4
; Sequence 4, Application US/08257073
; Patent No. 5766597
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  de Taisne, Charles
;    APPLICANT:  Tine, John A.
;    TITLE OF INVENTION:  MALARIA RECOMBINANT POXVIRUS VACCINE
;    NUMBER OF SEQUENCES:  143
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
;      STREET:  530 Fifth Avenue, 25th Floor
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  UNITED STATES OF AMERICA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/257,073
;      FILING DATE:  09-JUN-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/075,783
;      FILING DATE:  11-JUN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/852,305
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/672,183
;      FILING DATE:  20-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2570
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066 CURTMS
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2223 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-257-073-4

  Query Match             3.1%;  Score 43.2;  DB 1;  Length 2223;
  Best Local Similarity   63.5%;  Pred. No. 0.058;
  Matches   66;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy       1286 TCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGA 1345
             | || | | | |||||| ||  |||   ||| ||| ||   ||| || | |   | | |
Db       1488 TGTTATGGATGAAATTGATTTCTTTGAAAAAGAATTAATCGAAAATAATAATACACCTAA 1547

Qy       1346 TGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAAAAAAAAAAA 1389
              ||||  ||  | |||||   |  ||||||||| |||||  |||
Db       1548 TGTTGTACCACCAACTCAATCAAAAAAAAAAAACAAAAATGAAA 1591


RESULT 6
US-09-601-537-10
; Sequence 10, Application US/09601537
; Patent No. 6582691
; GENERAL INFORMATION:
;  APPLICANT: Gallert, Karl-Christian
;  APPLICANT:  Mullner, Stefan
;  APPLICANT:  Huls, Christoph
;  APPLICANT:  Bohnisch, Britta
;  TITLE OF INVENTION: Expression Vector for the Production of
;  TITLE OF INVENTION:  Dead Proteins
;  FILE REFERENCE: 50186/002001
;  CURRENT APPLICATION NUMBER: US/09/601,537
;  CURRENT FILING DATE:  2000-08-02
;  PRIOR APPLICATION NUMBER: PCT/EP99/00829
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: DE 198 05 781.4
;  PRIOR FILING DATE: 1998-02-12
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: p153-NT3
US-09-601-537-10

  Query Match             3.1%;  Score 43;  DB 4;  Length 441;
  Best Local Similarity   48.9%;  Pred. No. 0.026;
  Matches  115;  Conservative    0;  Mismatches  120;  Indels    0;  Gaps    0;

Qy       1156 TGAGCCAGGACCTGGGGCGGGGGTGGGGCCGGGGCCTTTCTGCCTCATTTGCTTTCAATG 1215
             ||  |||||||    || |   | | | |  ||   |  ||| ||  |||  |     ||
Db        176 TGGCCCAGGACACTTGGTGTATGCGTGACTTGGCTGTGGCTGTCTTTTTTAATCCTTGTG 235

Qy       1216 AAAGCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAAT 1275
              ||  |   ||  |       |   ||  ||      ||  |      || |  ||   |||
Db        236 TAAAGCAGCAAAAAAGACCTAAAGGGAATTGTAATTTGGTTATAATTCAGGATTTGGAAA 295

Qy       1276 CTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTT 1335
              | || |  ||||      |||       | | |   |||||| |||| ||||  |
Db        296 TAAATTTATTATTTGTAAAACAAAAAAAAAAATCTCCAAAAAAAAAAAAAAAAAAAAAAA 355

Qy       1336 AATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAAAAAAAAAAA 1390
              || |||| |      | |  |||          ||||||||||||||||||||
Db        356 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 410
```

```
RESULT 7
US-08-906-769-82
; Sequence 82, Application US/08906769
; Patent No. 6077687
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/906,769
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/639,075
;      FILING DATE:  24-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  944 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..768
US-08-906-769-82

  Query Match             3.1%;  Score 43;  DB 3;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| |||||  ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             |  | | |||  | |  ||||| |||  |  ||    |||   |    |   |||||||
Db        874 TTTATTCAAACGAATGTATAAAGTGAATTAACAATAAAAATGTTAGTGTTGCCAAAAAAA 933

Qy       1380 AAAAAAAAAAA 1390
             |||||||||||
Db        934 AAAAAAAAAAA 944


RESULT 8
US-08-906-616-82
; Sequence 82, Application US/08906616
; Patent No. 6121035
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/906,616
;      FILING DATE:  05-AUG-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C2-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  944 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..768
US-08-906-616-82

  Query Match             3.1%;  Score 43;  DB 3;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| |||||  ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             |  | | |||  | |  ||||| |||  |  ||    |||   |    |   |||||||
Db        874 TTTATTCAAACGAATGTATAAAGTGAATTAACAATAAAAATGTTAGTGTTGCCAAAAAAA 933

Qy       1380 AAAAAAAAAAA 1390
             |||||||||||
Db        934 AAAAAAAAAAA 944


RESULT 9
US-08-817-795-82
; Sequence 82, Application US/08817795
; Patent No. 6139840
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Hunter, Shirley Wu
```

```
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Heath, Andrew W.
;    APPLICANT:  Yamaka, Miles Yamanaka
;    APPLICANT:  Arfsten, Ann
;    APPLICANT:  Dale, Beverly
;    APPLICANT:  Stiegler, Gary
;    TITLE OF INVENTION:  USE OF PROTEASE INHIBITORS AND
;    TITLE OF INVENTION:  PROTEASE VACCINES TO PROTECT  ANIMALS FROM FLEA
;    TITLE OF INVENTION:  INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  119
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,795
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14442
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gary J. Connell
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303 863-0223
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  944 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..768
US-08-817-795-82

  Query Match             3.1%;  Score 43;  DB 3;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| |||||  ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             |  | | |||  | |  ||||| |||  |  ||    |||   |     |    |||||||
Db        874 TTTATTCAAACGAATGTATAAAGTGAATTAACAATAAAAATGTTAGTGTTGCCAAAAAAA 933

Qy       1380 AAAAAAAAAAA 1390
             ||||||||||
Db        934 AAAAAAAAAAA 944


RESULT 10
US-08-639-075A-82
; Sequence 82, Application US/08639075A
; Patent No. 6150125
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/639,075A
;      FILING DATE:  24-APR-1996
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  944 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..768
US-08-639-075A-82

  Query Match             3.1%;  Score 43;  DB 3;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| |||||  ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             |  | | |||  | |  ||||| |||  |  ||    |||   |     |    |||||||
Db        874 TTTATTCAAACGAATGTATAAAGTGAATTAACAATAAAAATGTTAGTGTTGCCAAAAAAA 933

Qy       1380 AAAAAAAAAAA 1390
             ||||||||||
Db        934 AAAAAAAAAAA 944


RESULT 11
US-09-012-431-82
; Sequence 82, Application US/09012431
; Patent No. 6180383
;  GENERAL INFORMATION:
;       APPLICANT: Grieve, Robert B.
;                  Rushlow, Keith E.
;                  Wu Hunter, Shirley
;                  Frank, Glenn R.
;                  Stiegler, Gary
;                  Gaines, Patrick J.
;                  Silver, Gary
;       TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
```

```
;                          MOLECULES AND USES THEREOF
;       NUMBER OF SEQUENCES: 190
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Sheridan Ross & McIntosh
;            STREET: 1700 Lincoln Street, Suite 3500
;            CITY: Denver
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80203
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/012,431
;            FILING DATE: 23-Jan-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/639,075
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Connell, Gary J.
;            REGISTRATION NUMBER: 32,020
;            REFERENCE/DOCKET NUMBER: 2618-25-C2
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (303) 863-9700
;            TELEFAX: (303) 863-0223
;   INFORMATION FOR SEQ ID NO: 82:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 944 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  3..768
;       SEQUENCE DESCRIPTION: SEQ ID NO: 82:
US-09-012-431-82

  Query Match             3.1%;  Score 43;  DB 3;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| |||||  ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             |  | | |||  | |  ||||| |||  |  ||    |||   |    |    |||||||
Db        874 TTTATTCAAACGAATGTATAAAGTGAATTAACAATAAAAATGTTAGTGTTGCCAAAAAAA 933

Qy       1380 AAAAAAAAAAA 1390
             |||||||||||
Db        934 AAAAAAAAAAA 944


RESULT 12
US-09-012-692-82
; Sequence 82, Application US/09012692
; Patent No. 6214579
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/012,692
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/639,075
;      FILING DATE:  24-APR-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Connell, Gary J.
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:  2618-25-C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303) 863-0223
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  944 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..768
US-09-012-692-82

  Query Match             3.1%;  Score 43;  DB 3;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| |||||  ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             |  | | |||  | |  ||||| |||  |  ||    |||   |    |    |||||||
Db        874 TTTATTCAAACGAATGTATAAAGTGAATTAACAATAAAAATGTTAGTGTTGCCAAAAAAA 933

Qy       1380 AAAAAAAAAAA 1390
             |||||||||||
Db        934 AAAAAAAAAAA 944


RESULT 13
US-08-906-613-82
; Sequence 82, Application US/08906613
; Patent No. 6232096
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wu Hunter, Shirley
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Stiegler, Gary
;    APPLICANT:  Gaines, Patrick J.
;    APPLICANT:  Silver, Gary
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES AND USES THEREOF
;    NUMBER OF SEQUENCES:  190
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
```

```
;       CITY:  Denver
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80203
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/906,613
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/639,075
;       FILING DATE:  24-APR-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Connell, Gary J.
;       REGISTRATION NUMBER:  32,020
;       REFERENCE/DOCKET NUMBER:  2618-25-C2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 863-9700
;       TELEFAX:  (303) 863-0223
;   INFORMATION FOR SEQ ID NO:  82:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  944 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  3..768
US-08-906-613-82

  Query Match             3.1%;  Score 43;  DB 3;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| ||||| ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             |  | | |||  | |  ||||| ||| |  ||    |||   |    |   |||||||
Db        874 TTTATTCAAACGAATGTATAAAGTGAATTAACAATAAAAATGTTAGTGTTGCCAAAAAAA 933

Qy       1380 AAAAAAAAAAA 1390
             |||||||||||
Db        934 AAAAAAAAAAA 944


RESULT 14
PCT-US95-14442A-82
; Sequence 82, Application PC/TUS9514442A
;  GENERAL INFORMATION:
;    APPLICANT:  Grieve, Robert B.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Hunter, Shirley Wu
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Heath, Andrew W.
;    APPLICANT:  Yamaka, Miles Yamanaka
;    APPLICANT:  Arfsten, Ann
;    APPLICANT:  Dale, Beverly
;    APPLICANT:  Stiegler, Gary
;    TITLE OF INVENTION:  USE OF PROTEASE INHIBITORS AND
;    TITLE OF INVENTION:  PROTEASE VACCINES TO PROTECT  ANIMALS FROM FLEA
;    TITLE OF INVENTION:  INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
;    TITLE OF INVENTION:  MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  119
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross & McIntosh
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/14442A
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gary J. Connell
;      REGISTRATION NUMBER:  32,020
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 863-9700
;      TELEFAX:  (303 863-0223
;  INFORMATION FOR SEQ ID NO:  82:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  944 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3..768
PCT-US95-14442A-82

  Query Match             3.1%;  Score 43;  DB 5;  Length 944;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy       1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             ||| | |||    |||| ||||| ||| ||    |    | ||||||| | ||   |
Db        814 TTTTAGTATAATAAATCCTTTGTGATTCATGCAAATATTTTGTTTTATTTATTTATTTAC 873

Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
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RESULT 15
US-09-032-215-26
; Sequence 26, Application US/09032215
; Patent No. 6204010
;  GENERAL INFORMATION:
;    APPLICANT:  Stiegler, Gary L.
;    APPLICANT:  Gaines, Patrick J.
;    TITLE OF INVENTION:  FLEA PROTEASE PROTEINS, NUCLEIC
;    TITLE OF INVENTION:  ACID MOLECULES, AND USES THEREOF
;    NUMBER OF SEQUENCES:  50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sheridan Ross P.C.
;      STREET:  1700 Lincoln Street, Suite 3500
;      CITY:  Denver
;      STATE:  Colorado
;      COUNTRY:  U.S.A.
;      ZIP:  80203
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII DOS TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/032,215
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;       FILING DATE:  27-FEB-1998
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Connell, Gary J.
;       REGISTRATION NUMBER:  32,020
;       REFERENCE/DOCKET NUMBER:  2618-25-C6
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (303) 863-9700
;       TELEFAX:  (303) 863-0223
;   INFORMATION FOR SEQ ID NO:  26:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  945 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..768
US-09-032-215-26

  Query Match             3.1%;  Score 43;  DB 3;  Length 945;
  Best Local Similarity   58.0%;  Pred. No. 0.04;
  Matches   76;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

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Qy       1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
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Qy       1380 AAAAAAAAAAA 1390
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Job time : 82 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 19:04:07 ; Search time 358 Seconds
(without alignments)
12969.464 Million cell updates/sec

Title: US-09-989-919-15
Perfect score: 1397
Sequence: 1 ggtgctgcacctgtaccgga.....aaaaaaaaaaaaaggcggtc 1397

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	940.4	67.3	1714	13	US-10-006-285-474	Sequence 474, App
3	464.2	33.2	470	10	US-09-989-919-14	Sequence 14, Appl
c 4	420.8	30.1	427	10	US-09-880-107-1138	Sequence 1138, Ap
5	164	11.7	1358	13	US-10-006-285-304	Sequence 304, App
6	97	6.9	493	11	US-09-918-995-32213	Sequence 32213, A
7	72.2	5.2	250	13	US-10-006-285-33	Sequence 33, Appl
c 8	55.2	4.0	428	10	US-09-960-352-10180	Sequence 10180, A
c 9	53.8	3.9	664	13	US-09-814-353-4739	Sequence 4739, Ap
c 10	53.8	3.9	664	13	US-09-814-353-11036	Sequence 11036, A
c 11	53.6	3.8	476	13	US-09-814-353-17420	Sequence 17420, A
c 12	52.4	3.8	383	13	US-09-814-353-18006	Sequence 18006, A
13	51	3.7	375	10	US-09-960-352-15014	Sequence 15014, A
c 14	50.6	3.6	425	10	US-09-834-975-451	Sequence 451, App
c 15	50.6	3.6	16688	13	US-10-311-455-293	Sequence 293, App
c 16	50.4	3.6	317	13	US-10-125-968-1260	Sequence 1260, Ap
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c 19	50.2	3.6	302	13	US-09-814-353-11622	Sequence 11622, A
c 20	50	3.6	461	13	US-09-814-353-17779	Sequence 17779, A
c 21	49.4	3.5	312	10	US-09-960-352-8414	Sequence 8414, Ap
c 22	49	3.5	361	15	US-10-198-846-8619	Sequence 8619, Ap
c 23	48.8	3.5	375	10	US-09-960-352-15014	Sequence 15014, A
c 24	48.8	3.5	424	10	US-09-960-352-11218	Sequence 11218, A
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c 26	48.4	3.5	298	10	US-09-960-352-1004	Sequence 1004, Ap
c 27	48.2	3.5	348	13	US-09-814-353-5612	Sequence 5612, Ap
c 28	48.2	3.5	348	13	US-09-814-353-11899	Sequence 11899, A
c 29	48.2	3.5	436	10	US-09-834-975-533	Sequence 533, App
30	48.2	3.5	1885	13	US-09-814-353-19371	Sequence 19371, A
c 31	48.2	3.5	8260	13	US-10-240-453-215	Sequence 215, App
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c 33	48	3.4	530	13	US-09-814-353-5294	Sequence 5294, Ap
c 34	48	3.4	530	13	US-09-814-353-11581	Sequence 11581, A
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36	47.8	3.4	312	10	US-09-960-352-8414	Sequence 8414, Ap
c 37	47.6	3.4	435	13	US-09-814-353-5103	Sequence 5103, Ap
c 38	47.6	3.4	435	13	US-09-814-353-11395	Sequence 11395, A
c 39	47.2	3.4	403	10	US-09-960-352-3319	Sequence 3319, Ap
c 40	47	3.4	638	15	US-10-198-846-8560	Sequence 8560, Ap
c 41	46.8	3.4	600	15	US-10-198-846-8434	Sequence 8434, Ap
c 42	46.8	3.4	1767	14	US-10-001-843-1	Sequence 1, Appli
43	46.6	3.3	416	10	US-09-960-352-4584	Sequence 4584, Ap
c 44	46.4	3.3	346	13	US-09-814-353-17676	Sequence 17676, A
c 45	46.2	3.3	418	10	US-09-960-352-4845	Sequence 4845, Ap

ALIGNMENTS

RESULT 1
US-09-989-919-15
; Sequence 15, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pr
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1397
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-919-15

Query Match 100.0%; Score 1397; DB 10; Length 1397;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATC 120

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Db        121 CTACCACCACGGGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTG 180

Qy        181 TGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGA 240
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Qy        241 GCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAGATAG 300
Db        241 GCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAGATAG 300

Qy        301 TGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGTGTCT 360
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Qy        361 TCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGCCCTG 420
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Qy        421 TTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGGAGCC 480
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Qy        661 GACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCAG 720
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Qy        781 ACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCT 840
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Qy       1321 AAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAA 1380
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Qy       1381 AAAAAAAAAAGGCGGTC 1397
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RESULT 2
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; Sequence 474, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
;  APPLICANT: Mary Jane Cunningham
;  APPLICANT:  Matthew R. Kaser
;  TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
;  FILE REFERENCE: PA-0039 US
;  CURRENT APPLICATION NUMBER: US/10/006,285
;  CURRENT FILING DATE:  2001-12-05
;  NUMBER OF SEQ ID NOS: 514
;  SOFTWARE: PERL Program
; SEQ ID NO 474
;   LENGTH: 1714
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030165854A1 018653.18
US-10-006-285-474

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  Best Local Similarity  84.7%;  Pred. No. 2.6e-238;
  Matches 1159;  Conservative    0;  Mismatches    1;  Indels  208;  Gaps    1;

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Qy       1021 TGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAGGGGACACTCCCAG 1080
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RESULT 3
US-09-989-919-14
; Sequence 14, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prd
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-919-14

Query Match 33.2%; Score 464.2; DB 10; Length 470;
Best Local Similarity 99.4%; Pred. No. 1.7e-112;
Matches 466; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy        567 CAGCAGCTGGGCTTGCCTGTGGAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTG 626
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CAGGTGCTGGGCTTGCCTGTGGAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTG 61

Qy        627 GGAACCCCTGCAGACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GGAACCCCTGCAGACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGC 121

Qy        687 AATAATGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AATAATGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTA 181

Qy        747 GTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAG 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAG 241

Qy        807 GCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATC 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATC 301

Qy        867 ACTGTGTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCA 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ACTGTGTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCA 361

Qy        927 CAGCAGGCGGTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGT 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 CAGCAGGCGGTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGT 421

Qy        987 CTGGACAGGAGACTTGGCGGGGGATGCTCCAGGATGTGGGTGATTCTGT 1035
              ||||||||||||||||||||||||||| ||||||||||||||||||||
Db        422 CTGGACAGGAGACTTGGCGGGGGATGCCCCAGGATGTGGGTGATTCTGT 470
```

RESULT 4
US-09-880-107-1138/c
; Sequence 1138, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1138
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens

```
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA451877
US-09-880-107-1138

  Query Match             30.1%;  Score 420.8;  DB 10;  Length 427;
  Best Local Similarity   99.5%;  Pred. No. 5.1e-101;
  Matches  422;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        936 GTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGG 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGG 368

Qy        996 AGACTTGGCGGGGGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTG 1055
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        367 AGACTTGGCGGGAGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTG 308

Qy       1056 ACCTCCCGACAGGGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCT 1115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACCTCCCGACAGGGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCT 248

Qy       1116 CAGCATGAGCCAAGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGG 1175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CAGCATGAGCCAAGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGG 188

Qy       1176 GGGTGGGGCCGGGGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAA 1235
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGGTGGGACCGGGGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAA 128

Qy       1236 ACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGT 1295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGT 68

Qy       1296 TAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAG 1355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAG 8

Qy       1356 CAAA 1359
              ||||
Db          7 CAAA 4


RESULT 5
US-10-006-285-304
; Sequence 304, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
;  APPLICANT: Mary Jane Cunningham
;  APPLICANT:  Matthew R. Kaser
;  TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
;  FILE REFERENCE: PA-0039 US
;  CURRENT APPLICATION NUMBER: US/10/006,285
;  CURRENT FILING DATE:  2001-12-05
;  NUMBER OF SEQ ID NOS: 514
;  SOFTWARE: PERL Program
; SEQ ID NO 304
;   LENGTH: 1358
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030165854A1 218659_Rn.1
US-10-006-285-304

  Query Match             11.7%;  Score 164;  DB 13;  Length 1358;
  Best Local Similarity   84.0%;  Pred. No. 1.2e-32;
  Matches  210;  Conservative    0;  Mismatches   35;  Indels    5;  Gaps    2;

Qy          1 GGTGCTGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTAC 60
              || |||||||||||| |||||| |||||||| |||||||||||| |   |||||||||| |
Db        260 GGCGCTGCACCTGTTCCGGAGTGGGCAGTACCTGCAGAACTCTA---CAAGCAGCAGGGC 316

Qy         61 CGAGTACCAGTGTATCCCAGAC--AGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCA 118
              ||||||||| | ||||| |||  |  |||||| | ||||| || || ||||||||||

Db        317 TGAGTACCAGCGCATCCCGGACAAATTACCATCACACAGGAGGATTATCGCTGCTGGCCC 376

Qy        119 TCCTACCACCACGGGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTC 178
              |||||||||||| ||  |||||||||| || |||||||||||||||||||| ||||||
Db        377 TCCTACCACCATGGTGGCTGCCTCCTGTCTGTGTTCAACCTGGCTGAGGCTGTAGATGTC 436

Qy        179 TGTGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGT 238
              |||||||||||||  || ||||| ||||||||||||||||||||||||||||||||||||
Db        437 TGTGAGAGCCATGTTCAATGTCGTGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGT 496

Qy        239 GAGCCAGTGG 248
                 |   |||
Db        497 CGGAAGCTGG 506


RESULT 6
US-09-918-995-32213
; Sequence 32213, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32213
;   LENGTH: 493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(493)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32213

  Query Match              6.9%;  Score 97;  DB 11;  Length 493;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-15;
  Matches   97;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGTGCTGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GGTGCTGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTAC 456

Qy         61 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAG 97
              |||||||||||||||||||||||||||||||||||||
Db        457 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAG 493


RESULT 7
US-10-006-285-33
; Sequence 33, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
;  APPLICANT: Mary Jane Cunningham
;  APPLICANT:  Matthew R. Kaser
;  TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
;  FILE REFERENCE: PA-0039 US
;  CURRENT APPLICATION NUMBER: US/10/006,285
;  CURRENT FILING DATE:  2001-12-05
;  NUMBER OF SEQ ID NOS: 514
;  SOFTWARE: PERL Program
; SEQ ID NO 33
;   LENGTH: 250
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030165854A1 700175249H1
```

US-10-006-285-33

Query Match 5.2%; Score 72.2; DB 13; Length 250;
Best Local Similarity 63.6%; Pred. No. 8.3e-09;
Matches 110; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

```
Qy        590 GGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCAGACAAAGCTAA 649
              ||| || ||    | |||   |||         |  || | |||||||||||| |||||
Db         49 GGGTTTGCCTGCTGCAGGCGTGACTTGCATAGCACCCGGGAACCCTGCAGACAGAGCTAG 108

Qy        650 CATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGT 709
              | |||||||   || ||||||||||||||||||||||||||     || ||||||||||
Db        109 CGTCCCAGAGCAACTGATGTGACCAGGACAAACGTGCAATATGCAAAAGTGTTAAAATGT 168

Qy        710 GAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGG 762
              |||||| ||||| |               | ||||| || |   |  |||  ||
Db        169 GAGTTTGCCAGCTTTCGGTCTAAGACTGTTGCTCCCAGCCTGAGCGTCACTGG 221
```

RESULT 8
US-09-960-352-10180/c
; Sequence 10180, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 10180
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 44-LIB188-026-Q1-E1-C12
US-09-960-352-10180

Query Match 4.0%; Score 55.2; DB 10; Length 428;
Best Local Similarity 70.5%; Pred. No. 0.00038;
Matches 117; Conservative 0; Mismatches 43; Indels 6; Gaps 3;

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Qy        903 CTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCGTGGGGACAATCCATC 962
              |||||| |||||||||| |||||  ||   | |  ||||| ||| ||||||||||  ||
Db        427 CTGCTGGTGCTGCTGCATGTGCCATGGC--TCAGCAGGGGCCGCGAGGGGACAATCGGTC 370

Qy        963 GTGGAG--TGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGGGGATGCTCCAGGA 1020
               |||||   |||||||  |||  || ||  ||  |||||||||    |||||||||||  ||
Db        369 ATGGAGCACGTTCTCTTAGCCAAGCTCCTGAGCGGAGACTTGAA--GGGATGCTCCAAGA 312

Qy       1021 TGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACA 1066
              |||||| ||||||||||  | |       | ||| ||  ||  ||
Db        311 TGTGGGCGATTCTGTACCGCGTGGTCAGCGCCCTGCCCATCCAGCA 266
```

RESULT 9
US-09-814-353-4739/c
; Sequence 4739, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4739
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 53, 54, 159, 161, 174, 177, 178, 180, 182, 185, 212, 215,
; LOCATION: 216, 219, 220, 226, 237, 247, 248, 265, 269, 278, 281, 283,
; LOCATION: 289, 294, 298, 299, 300, 301, 302, 304, 305, 307, 308, 316,
; LOCATION: 327, 333, 334, 335, 336, 339, 343, 344, 345, 348, 368
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 377, 383, 386, 388, 390, 409, 429, 431, 433, 439, 447, 450,
; LOCATION: 452, 460, 462, 473, 474, 475, 477, 484, 486, 508, 509, 510,
; LOCATION: 511, 513, 514, 515, 518, 519, 520, 522, 525, 528, 530, 532,
; LOCATION: 533, 541, 542, 543, 544, 547, 550, 552, 561, 564, 570
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 573, 575, 578, 584, 600, 601, 603, 606, 607, 616, 623, 625,
; LOCATION: 626, 642
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-4739

Query Match 3.9%; Score 53.8; DB 13; Length 664;
Best Local Similarity 55.4%; Pred. No. 0.0012;
Matches 82; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

```
Qy       1243 TTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTG 1302
              | ||    || ||    |||     |   | ||| ||||    || || ||   |   |
Db        270 TNTCTNTTTTTCTTATTTTTTTNNAAAAAAAATNTTTTTGTTTTNTTCTTNNATNNTTNT 211

Qy       1303 TTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTC 1362
              ||| ||||| |  |||| |||| || || | |   |     |  | |||     |   | |
Db        210 TTTTTTTTTTTTTAAAAAAAAAAAAANATNANTNNTTNTTTTTTTTTTTTNTNCCCCCCCC 151

Qy       1363 TTCCCTAAAAAAAAAAAAAAAAAAAAAAA 1390
                |  ||||||||||||||||||||||
Db        150 CCCAAAAAAAAAAAAAAAAAAAAAAAAAA 123
```

RESULT 10
US-09-814-353-11036/c
; Sequence 11036, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25

```
;  PRIOR APPLICATION NUMBER: US 60/211,940
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: US 60/216,820
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 60/220,661
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: US 60/257,672
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 22037
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11036
;   LENGTH: 664
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 53, 54, 159, 161, 174, 177, 178, 180, 182, 185, 212, 215,
;   LOCATION: 216, 219, 220, 226, 237, 247, 248, 265, 269, 278, 281, 283,
;   LOCATION: 289, 294, 298, 299, 300, 301, 302, 304, 305, 307, 308, 316,
;   LOCATION: 327, 333, 334, 335, 336, 339, 343, 344, 345, 348, 368
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 377, 383, 386, 388, 390, 409, 429, 431, 433, 439, 447, 450,
;   LOCATION: 452, 460, 462, 473, 474, 475, 477, 484, 486, 508, 509, 510,
;   LOCATION: 511, 513, 514, 515, 518, 519, 520, 522, 525, 528, 530, 532,
;   LOCATION: 533, 541, 542, 543, 544, 547, 550, 552, 561, 564, 570
;   OTHER INFORMATION: n = A,T,C or G
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 573, 575, 578, 584, 600, 601, 603, 606, 607, 616, 623, 625,
;   LOCATION: 626, 642
;   OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11036

  Query Match             3.9%;  Score 53.8;  DB 13;  Length 664;
  Best Local Similarity   55.4%;  Pred. No. 0.0012;
  Matches   82;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy       1243 TTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTG 1302
             | ||    || ||    |||     |   | ||| ||||    || || ||   |   |
Db        270 TNTCTNTTTTTCTTATTTTTTTNNAAAAAAAATNTTTTTGTTTTNTTCTTNNATNNTTNT 211

Qy       1303 TTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTC 1362
             ||| ||||| |  |||| |||| || || | |   |     |  | |||      |   | |
Db        210 TTTTTTTTTTTTTAAAAAAAAAAAAANATNANTNNTTNTTTTTTTTTTTTNTNCCCCCCCC 151

Qy       1363 TTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
                |   ||||||||||||||||||||||
Db        150 CCCAAAAAAAAAAAAAAAAAAAAAAAAA 123


RESULT 11
US-09-814-353-17420/c
; Sequence 17420, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, John
;  APPLICANT:  Thompson, Pamela
;  APPLICANT:  Lillie, James
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF OVARIAN CANCER
;  FILE REFERENCE: MRI-006B
;  CURRENT APPLICATION NUMBER: US/09/814,353
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: US 60/191,031
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/207,124
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: US 60/211,940
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: US 60/216,820
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 60/220,661
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: US 60/257,672
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 22037
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17420
;   LENGTH: 476
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-814-353-17420

  Query Match             3.8%;  Score 53.6;  DB 13;  Length 476;
  Best Local Similarity   57.9%;  Pred. No. 0.0011;
  Matches   95;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy       1227 GCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTT 1286
             | ||  |||| |     || |  ||  |     ||| | |   | ||| ||||    ||
Db        342 GGAGGAAAAAAAAAAAAACTCTCTTTTTATTATTTTTTTAAAAAAAAAATATTTTTGTTTT 283

Qy       1287 CTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGAT 1346
             ||| ||    || || ||| ||||| |  |||| |||| ||||| | ||  |    |  |
Db        282 CTTCTTCAAAAACTTTTTTTTTTTTTTTTAAAAAAAAAAAAAATAAATTTTTTTTTTTTT 223

Qy       1347 GTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              |||      |  | |  | · ||||||||||||||||||||
Db        222 TTTTTGGCCCCCCCCCCCCAAAAAAAAAAAAAAAAAAAAAAAA 179


RESULT 12
US-09-814-353-18006/c
; Sequence 18006, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, John
;  APPLICANT:  Thompson, Pamela
;  APPLICANT:  Lillie, James
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF OVARIAN CANCER
;  FILE REFERENCE: MRI-006B
;  CURRENT APPLICATION NUMBER: US/09/814,353
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: US 60/191,031
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/207,124
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: US 60/211,940
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: US 60/216,820
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 60/220,661
;  PRIOR FILING DATE: 2000-07-25
;  PRIOR APPLICATION NUMBER: US 60/257,672
;  PRIOR FILING DATE: 2000-12-21
;  NUMBER OF SEQ ID NOS: 22037
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18006
;   LENGTH: 383
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-814-353-18006

  Query Match             3.8%;  Score 52.4;  DB 13;  Length 383;
  Best Local Similarity   61.9%;  Pred. No. 0.0019;
  Matches   83;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy       1259 GTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAA 1318
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Db        212 GTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTAAAAAA 153

Qy       1319 ATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAA 1378
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Db       152 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTTAAAAAAAAAA 93

Qy      1379 AAAAAAAAAAAAGG 1392
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Db        92 AAAAAAAAAAAAAG 79


RESULT 13
US-09-960-352-15014
; Sequence 15014, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
;  APPLICANT: Warren, Wesley C.
;  APPLICANT:  Tao, Nengbing
;  APPLICANT:  Byatt, John C.
;  APPLICANT:  Mathialagan, Nagappan
;  TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
;  TITLE OF INVENTION:  MUSCLE AND FAT DEPOSITION
;  FILE REFERENCE: 16511.006/37-21(10298)C
;  CURRENT APPLICATION NUMBER: US/09/960,352
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 15014
;   LENGTH: 375
;   TYPE: DNA
;   ORGANISM: Bos taurus
;   OTHER INFORMATION: Clone ID: 64-LIB3058-048-Q1-K1-H8
US-09-960-352-15014

  Query Match             3.7%;  Score 51;  DB 10;  Length 375;
  Best Local Similarity   61.8%;  Pred. No. 0.0045;
  Matches   81;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy      1260 TTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAA 1319
             |||   | |  |  || |||| || || || ||  ||  ||| ||| || || |||||||
Db       131 TTTTTTTTTTTATTATTTTTTTTATTTATTTTTATTTTTATTATTTTTTATTTTAAAAAA 190

Qy      1320 TAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAA 1379
             ||||| ||||  |   || | |   || |||     |||       |||||||||
Db       191 TAAAAAAAAAAAAAAAAAAATATATATTTTTTTTTTAAAAAAAAGGATGGAAAAAAAAAT 250

Qy      1380 AAAAAAAAAAA 1390
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Db       251 AAAAAAAAAAA 261


RESULT 14
US-09-834-975-451/c
; Sequence 451, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
;  APPLICANT: Lillie, James
;  APPLICANT:  Brown, Jeffrey
;  APPLICANT:  Bolt, Andrew
;  APPLICANT:  Van Huffel, Christophe
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
;  TITLE OF INVENTION:  FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
;  TITLE OF INVENTION:  OF HUMAN CANCERS
;  FILE REFERENCE: MRI-016B
;  CURRENT APPLICATION NUMBER: US/09/834,975
;  CURRENT FILING DATE:  2001-04-13
;  PRIOR APPLICATION NUMBER: 60/197,538
;  PRIOR FILING DATE: 2000-04-14
;  NUMBER OF SEQ ID NOS: 1046
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 451
;   LENGTH: 425
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(425)
;   OTHER INFORMATION: n = A,T,C or G
US-09-834-975-451

  Query Match             3.6%;  Score 50.6;  DB 10;  Length 425;
  Best Local Similarity   53.7%;  Pred. No. 0.0062;
  Matches  101;  Conservative    0;  Mismatches   87;  Indels    0;  Gaps    0;

Qy      1203 TTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTT 1262
             |||  |||   | |||     |   |  |  ||||  |       |||  ||  |    |||
Db       223 TTTTTTTTTTTTAAAAAAAACGGGGGGGGGAAAAAAAAAAAAACCCTTTTTTTTTTTTTT 164

Qy      1263 GAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAA 1322
                |   | |||| |  || || ||  | ||||| ||| ||||| |   ||| ||
Db       163 TGGGGGAAATTTTTTTTTTTTTTTTTTTTTTTAAAATTTTTTTTTTTTTTTNNNAAAAAA 104

Qy      1323 AATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAAA 1382
             || |||| |   || |||| |       | |  |||         ||||||||||||||
Db       103 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44

Qy      1383 AAAAAAAA 1390
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Db        43 AAAAAAAA 36


RESULT 15
US-10-311-455-293/c
; Sequence 293, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
;  APPLICANT: OLEK, Alexander
;  APPLICANT:  PIEPENBROCK, Christian
;  APPLICANT:  BERLIN, Kurt
;  TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deterr
;  TITLE OF INVENTION:  cytosine methylation
;  FILE REFERENCE: 5013.1014
;  CURRENT APPLICATION NUMBER: US/10/311,455
;  CURRENT FILING DATE:  2002-12-16
;  PRIOR APPLICATION NUMBER: PCT/EP01/07537
;  PRIOR FILING DATE: 2001-07-02
;  PRIOR APPLICATION NUMBER: DE 10032529.7
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: DE 10043826.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 293
;   LENGTH: 16688
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-293

  Query Match             3.6%;  Score 50.6;  DB 13;  Length 16688;
  Best Local Similarity   53.9%;  Pred. No. 0.065;
  Matches  104;  Conservative    0;  Mismatches   89;  Indels    0;  Gaps    0;

Qy       1198 CCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCG 1257
              |||| ||| ||| |||| | |    |||  |   ||| |  |  | | || ||     |
Db      13638 CCTCCTTTCCTTACAATAATAAATACAATACTTACAATAATAATCCTACCGCCAATAACT 13579

Qy       1258 AGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAA 1317
              | |  |||||     |  | |  | |||||| ||  |     || ||| ||||| ||| |
Db      13578 TCTATATATATCTTTTAATTATCTTTCTTCTTCTTCTTCTTTTTTTTTTTTTTAATA 13519

Qy       1318 AATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAA 1377
              || || ||    |   || ||| ||      ||      ||||   | || | ||| |  |
Db      13518 TTTACAAAAACCATTAATACTAACATTTAAATTATTTCCAAAAATTACCTTTAAATACTA 13459

Qy       1378 AAAAAAAAAAAAA 1390
              | | |||| |||
Db      13458 TATATAAAACAAA 13446
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-989-919-15
Perfect score: 1397
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	27	1.9	775	4	US-09-220-132-191	Sequence 191, App
	3	27	1.9	1223	4	US-09-220-132-175	Sequence 175, App
	4	27	1.9	1817	1	US-08-473-981A-5	Sequence 5, Appli
	5	27	1.9	1817	2	US-08-474-087-5	Sequence 5, Appli
	6	27	1.9	2114	4	US-09-130-491-7	Sequence 7, Appli
c	7	27	1.9	99500	4	US-09-798-096-10	Sequence 10, Appl
c	8	26	1.9	511	4	US-09-328-475C-196	Sequence 196, App
	9	26	1.9	899	3	US-09-122-400B-11	Sequence 11, Appl
	10	26	1.9	1327	4	US-09-257-179-28	Sequence 28, Appl
	11	26	1.9	1509	4	US-09-620-312D-722	Sequence 722, App
	12	26	1.9	1569	4	US-09-482-273-51	Sequence 51, Appl
	13	26	1.9	1730	4	US-09-489-847-48	Sequence 48, Appl
	14	26	1.9	1758	3	US-08-836-567-3	Sequence 3, Appli
	15	26	1.9	1758	4	US-09-606-304-3	Sequence 3, Appli
	16	26	1.9	2093	1	US-08-287-001A-1	Sequence 1, Appli
	17	26	1.9	2093	5	PCT-US95-09941-1	Sequence 1, Appli
	18	26	1.9	2660	4	US-09-634-955B-1	Sequence 1, Appli
	19	26	1.9	3149	4	US-09-016-434-1453	Sequence 1453, Ap
	20	26	1.9	3289	4	US-09-904-615-11	Sequence 11, Appl
	21	26	1.9	3891	2	US-08-969-630-3	Sequence 3, Appli
c	22	26	1.9	8912	4	US-08-469-260A-11	Sequence 11, Appl
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c	24	26	1.9	8912	4	US-08-467-344A-11	Sequence 11, Appl
c	25	26	1.9	9143	2	US-08-639-857-32	Sequence 32, Appl
c	26	26	1.9	9143	4	US-08-469-260A-390	Sequence 390, App
c	27	26	1.9	9143	4	US-08-469-260A-393	Sequence 393, App
c	28	26	1.9	9143	4	US-08-488-446-390	Sequence 390, App
c	29	26	1.9	9143	4	US-08-488-446-393	Sequence 393, App
c	30	26	1.9	9143	4	US-08-467-344A-390	Sequence 390, App
c	31	26	1.9	9143	4	US-08-467-344A-393	Sequence 393, App
	32	26	1.9	14753	4	US-09-821-736-3	Sequence 3, Appli
	33	26	1.9	46718	4	US-09-816-093-3	Sequence 3, Appli
	34	26	1.9	152331	3	US-09-128-155-16	Sequence 16, Appl
	35	26	1.9	176373	3	US-09-128-155-17	Sequence 17, Appl
c	36	25	1.8	58	2	US-08-417-174-42	Sequence 42, Appl
c	37	25	1.8	58	2	US-08-231-565A-40	Sequence 40, Appl
c	38	25	1.8	58	2	US-09-007-961-40	Sequence 40, Appl
c	39	25	1.8	58	3	US-09-267-439-42	Sequence 42, Appl
c	40	25	1.8	58	4	US-09-073-138-42	Sequence 42, Appl
c	41	25	1.8	62	3	US-09-109-377-1	Sequence 1, Appli
	42	25	1.8	319	1	US-07-593-657-14	Sequence 14, Appl
c	43	25	1.8	506	3	US-09-328-111-746	Sequence 746, App
	44	25	1.8	523	2	US-08-628-413-1	Sequence 1, Appli
c	45	25	1.8	566	3	US-09-328-111-466	Sequence 466, App
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c	47	25	1.8	593	3	US-09-328-111-528	Sequence 528, App
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c	49	25	1.8	611	3	US-09-385-982-357	Sequence 357, App
	50	25	1.8	646	4	US-09-288-143-22	Sequence 22, Appl
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	52	25	1.8	889	1	US-08-661-168-4	Sequence 4, Appli
	53	25	1.8	940	4	US-09-091-097-11	Sequence 11, Appl
	54	25	1.8	1009	4	US-09-291-922-15	Sequence 15, Appl
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	56	25	1.8	1088	1	US-08-726-525-3	Sequence 3, Appli
	57	25	1.8	1088	1	US-08-487-942-3	Sequence 3, Appli
	58	25	1.8	1088	2	US-08-726-036A-3	Sequence 3, Appli
	59	25	1.8	1088	4	US-09-083-516-3	Sequence 3, Appli
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c	63	25	1.8	1181	1	US-08-444-803-27	Sequence 27, Appl
c	64	25	1.8	1181	1	US-08-449-043-27	Sequence 27, Appl
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c	67	25	1.8	1181	1	US-08-455-244-27	Sequence 27, Appl
c	68	25	1.8	1181	1	US-08-454-876-27	Sequence 27, Appl
c	69	25	1.8	1181	2	US-08-457-364-27	Sequence 27, Appl
c	70	25	1.8	1181	2	US-08-456-262-27	Sequence 27, Appl
c	71	25	1.8	1181	2	US-08-456-240-27	Sequence 27, Appl
c	72	25	1.8	1181	2	US-08-455-736-27	Sequence 27, Appl
c	73	25	1.8	1181	2	US-08-971-217-27	Sequence 27, Appl
c	74	25	1.8	1181	3	US-09-350-600-27	Sequence 27, Appl
c	75	25	1.8	1200	3	US-08-859-167-5	Sequence 5, Appli
c	76	25	1.8	1200	3	US-09-109-273-5	Sequence 5, Appli
c	77	25	1.8	1200	3	US-09-276-993-5	Sequence 5, Appli
c	78	25	1.8	1200	4	US-09-723-450-5	Sequence 5, Appli
	79	25	1.8	1225	4	US-09-216-393B-282	Sequence 282, App
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	81	25	1.8	1241	1	US-07-593-657-6	Sequence 6, Appli
	82	25	1.8	1241	3	US-08-942-012B-3	Sequence 3, Appli
	83	25	1.8	1274	3	US-08-335-844A-13	Sequence 13, Appl
	84	25	1.8	1274	4	US-09-129-366-13	Sequence 13, Appl
	85	25	1.8	1280	4	US-09-220-132-155	Sequence 155, App
	86	25	1.8	1283	1	US-07-885-970A-17	Sequence 17, Appl
	87	25	1.8	1283	1	US-08-298-687A-17	Sequence 17, Appl
	88	25	1.8	1283	1	US-08-530-797-18	Sequence 18, Appl
	89	25	1.8	1283	1	US-08-298-829-17	Sequence 17, Appl
	90	25	1.8	1283	2	US-08-787-335-18	Sequence 18, Appl
	91	25	1.8	1309	4	US-09-425-578-3	Sequence 3, Appli
	92	25	1.8	1564	4	US-09-489-847-11	Sequence 11, Appl
	93	25	1.8	1781	4	US-09-818-512-1	Sequence 1, Appli
	94	25	1.8	1829	3	US-08-688-988-9	Sequence 9, Appli
	95	25	1.8	1875	5	PCT-US96-10618-1	Sequence 1, Appli
	96	25	1.8	1921	3	US-08-840-767-51	Sequence 51, Appl
	97	25	1.8	1965	3	US-09-461-697-292	Sequence 292, App
	98	25	1.8	1992	3	US-08-840-767-1	Sequence 1, Appli
	99	25	1.8	2263	4	US-08-997-685A-9	Sequence 9, Appli
	100	25	1.8	2285	1	US-08-477-674-9	Sequence 9, Appli

	101	25	1.8	2285	1	US-08-473-791-9	Sequence 9, Appli
	102	25	1.8	2285	2	US-08-316-714-9	Sequence 9, Appli
	103	25	1.8	2285	3	US-08-473-673-9	Sequence 9, Appli
	104	25	1.8	2456	3	US-08-813-150-5	Sequence 5, Appli
	105	25	1.8	2456	4	US-09-546-553-5	Sequence 5, Appli
c	106	25	1.8	2672	1	US-08-703-947-1	Sequence 1, Appli
	107	25	1.8	2779	4	US-09-149-476-191	Sequence 191, App
	108	25	1.8	2861	2	US-08-770-301A-12	Sequence 12, Appl
	109	25	1.8	2861	3	US-09-175-581-12	Sequence 12, Appl
	110	25	1.8	2880	1	US-08-158-189-1	Sequence 1, Appli
	111	25	1.8	2907	3	US-09-232-200-52	Sequence 52, Appl
	112	25	1.8	2907	4	US-09-232-197-52	Sequence 52, Appl
	113	25	1.8	2907	4	US-09-232-201-52	Sequence 52, Appl
	114	25	1.8	2917	3	US-09-232-200-26	Sequence 26, Appl
	115	25	1.8	2917	4	US-09-232-197-26	Sequence 26, Appl
	116	25	1.8	2917	4	US-09-232-201-26	Sequence 26, Appl
c	117	25	1.8	3001	4	US-09-539-333D-153	Sequence 153, App
	118	25	1.8	3148	3	US-08-909-954-1	Sequence 1, Appli
c	119	25	1.8	4066	4	US-09-367-750-1	Sequence 1, Appli
c	120	25	1.8	4586	1	US-08-832-883-53	Sequence 53, Appl
c	121	25	1.8	4586	2	US-08-832-877-53	Sequence 53, Appl
c	122	25	1.8	4698	1	US-07-807-043B-5	Sequence 5, Appli
c	123	25	1.8	4698	1	US-08-299-849B-5	Sequence 5, Appli
c	124	25	1.8	4698	2	US-08-142-368A-5	Sequence 5, Appli
c	125	25	1.8	4698	3	US-08-967-727-5	Sequence 5, Appli
c	126	25	1.8	4698	3	US-08-037-230D-5	Sequence 5, Appli
c	127	25	1.8	4698	4	US-09-583-850-5	Sequence 5, Appli
c	128	25	1.8	4698	4	US-09-579-197-5	Sequence 5, Appli
c	129	25	1.8	4698	4	US-09-404-026-5	Sequence 5, Appli
c	130	25	1.8	8600	4	US-09-457-708-1	Sequence 1, Appli
c	131	25	1.8	8600	4	US-09-950-046A-1	Sequence 1, Appli
c	132	25	1.8	13187	4	US-09-422-936-61	Sequence 61, Appl
	133	25	1.8	36741	3	US-09-301-665-3	Sequence 3, Appli
c	134	25	1.8	43795	3	US-08-742-185-101	Sequence 101, App
c	135	25	1.8	51719	4	US-09-918-686-2	Sequence 2, Appli
c	136	25	1.8	65042	4	US-09-784-316-3	Sequence 3, Appli
	137	25	1.8	66804	4	US-09-740-041-3	Sequence 3, Appli
c	138	25	1.8	92139	4	US-09-918-686-1	Sequence 1, Appli
c	139	25	1.8	148567	4	US-09-801-876B-3	Sequence 3, Appli
c	140	25	1.8	174493	4	US-09-804-471A-3	Sequence 3, Appli
c	141	25	1.8	246240	2	US-08-724-394A-20	Sequence 20, Appl
c	142	25	1.8	246240	2	US-08-724-394A-21	Sequence 21, Appl
c	143	25	1.8	246240	2	US-08-724-394A-22	Sequence 22, Appl
	144	24	1.7	39	3	US-09-120-386-4	Sequence 4, Appli
	145	24	1.7	39	3	US-09-120-501-4	Sequence 4, Appli
	146	24	1.7	39	4	US-09-120-689-5	Sequence 5, Appli
	147	24	1.7	39	4	US-09-619-103-4	Sequence 4, Appli
	148	24	1.7	48	1	US-08-380-438-6	Sequence 6, Appli
	149	24	1.7	80	3	US-09-165-264-5	Sequence 5, Appli
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c	151	24	1.7	94	4	US-09-404-879A-261	Sequence 261, App
c	152	24	1.7	94	4	US-09-338-933-261	Sequence 261, App
c	153	24	1.7	94	4	US-09-215-681-261	Sequence 261, App
	154	24	1.7	104	2	US-08-803-899-8	Sequence 8, Appli
	155	24	1.7	140	1	US-08-628-417-5	Sequence 5, Appli
	156	24	1.7	153	3	US-09-244-794A-3	Sequence 3, Appli
	157	24	1.7	153	3	US-09-247-190-3	Sequence 3, Appli
	158	24	1.7	153	4	US-09-238-710-3	Sequence 3, Appli
	159	24	1.7	159	3	US-09-244-794A-17	Sequence 17, Appl
	160	24	1.7	159	3	US-09-247-190-17	Sequence 17, Appl
	161	24	1.7	159	4	US-09-238-710-17	Sequence 17, Appl
	162	24	1.7	216	1	US-08-686-878A-34	Sequence 34, Appl
	163	24	1.7	216	4	US-09-175-928-34	Sequence 34, Appl
	164	24	1.7	229	4	US-09-702-705-195	Sequence 195, App
	165	24	1.7	229	4	US-09-736-457-195	Sequence 195, App
	166	24	1.7	240	1	US-08-628-417-6	Sequence 6, Appli
	167	24	1.7	255	4	US-09-480-921B-26	Sequence 26, Appl
c	168	24	1.7	256	3	US-09-385-982-187	Sequence 187, App
c	169	24	1.7	256	3	US-09-385-982-387	Sequence 387, App
	170	24	1.7	277	1	US-08-244-113-18	Sequence 18, Appl
	171	24	1.7	288	2	US-08-648-496-1	Sequence 1, Appli
	172	24	1.7	314	3	US-09-277-016-37	Sequence 37, Appl
	173	24	1.7	314	4	US-09-883-548-7	Sequence 7, Appli
	174	24	1.7	314	4	US-09-883-717-7	Sequence 7, Appli
	175	24	1.7	314	4	US-09-757-949-7	Sequence 7, Appli
c	176	24	1.7	321	2	US-08-520-678A-23	Sequence 23, Appl
c	177	24	1.7	321	3	US-08-897-126-23	Sequence 23, Appl
c	178	24	1.7	325	2	US-08-541-033A-14	Sequence 14, Appl
c	179	24	1.7	325	2	US-08-828-451-14	Sequence 14, Appl
	180	24	1.7	326	4	US-09-629-645A-17	Sequence 17, Appl
	181	24	1.7	330	3	US-09-078-294-24	Sequence 24, Appl
	182	24	1.7	349	4	US-09-105-542A-6	Sequence 6, Appli
	183	24	1.7	361	2	US-08-465-380-39	Sequence 39, Appl
	184	24	1.7	361	2	US-08-486-397-39	Sequence 39, Appl
	185	24	1.7	361	2	US-08-486-399-39	Sequence 39, Appl
	186	24	1.7	361	2	US-08-461-965-39	Sequence 39, Appl
	187	24	1.7	361	2	US-08-634-641-39	Sequence 39, Appl
	188	24	1.7	361	3	US-09-249-471-39	Sequence 39, Appl
	189	24	1.7	361	3	US-09-249-472-39	Sequence 39, Appl
	190	24	1.7	361	3	US-09-249-451-39	Sequence 39, Appl
	191	24	1.7	361	3	US-08-809-455-39	Sequence 39, Appl
	192	24	1.7	361	3	US-09-249-461-39	Sequence 39, Appl
	193	24	1.7	361	3	US-09-249-448-39	Sequence 39, Appl
	194	24	1.7	361	4	US-09-249-473-39	Sequence 39, Appl
c	195	24	1.7	367	2	US-08-541-033A-13	Sequence 13, Appl
c	196	24	1.7	367	2	US-08-828-451-13	Sequence 13, Appl
c	197	24	1.7	374	3	US-09-385-982-494	Sequence 494, App
	198	24	1.7	433	1	US-07-987-272A-13	Sequence 13, Appl
	199	24	1.7	442	4	US-09-372-422A-35	Sequence 35, Appl
	200	24	1.7	452	4	US-09-397-787-237	Sequence 237, App
c	201	24	1.7	483	4	US-09-328-475C-239	Sequence 239, App
	202	24	1.7	487	4	US-09-257-179-22	Sequence 22, Appl
	203	24	1.7	488	4	US-09-480-251-1	Sequence 1, Appli
	204	24	1.7	499	4	US-09-328-475C-211	Sequence 211, App
c	205	24	1.7	500	2	US-08-967-101-82	Sequence 82, Appl
c	206	24	1.7	500	2	US-08-592-541-82	Sequence 82, Appl
c	207	24	1.7	500	3	US-09-124-698-82	Sequence 82, Appl
c	208	24	1.7	500	3	US-09-127-480-82	Sequence 82, Appl
c	209	24	1.7	500	3	US-08-496-841C-82	Sequence 82, Appl
c	210	24	1.7	500	4	US-09-124-523-82	Sequence 82, Appl
c	211	24	1.7	500	4	US-09-636-796A-82	Sequence 82, Appl
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	213	24	1.7	506	4	US-09-442-631-1	Sequence 1, Appli
	214	24	1.7	515	4	US-09-130-158A-3	Sequence 3, Appli
	215	24	1.7	541	4	US-09-288-143-50	Sequence 50, Appl
	216	24	1.7	569	4	US-09-461-325-44	Sequence 44, Appl
	217	24	1.7	578	4	US-09-461-325-87	Sequence 87, Appl
	218	24	1.7	585	3	US-08-938-548B-5	Sequence 5, Appli
	219	24	1.7	585	4	US-08-939-093A-5	Sequence 5, Appli
c	220	24	1.7	595	3	US-09-385-982-278	Sequence 278, App
	221	24	1.7	611	4	US-09-205-258-109	Sequence 109, App
c	222	24	1.7	623	3	US-09-385-982-207	Sequence 207, App
	223	24	1.7	628	4	US-09-227-357-104	Sequence 104, App
c	224	24	1.7	637	4	US-09-220-132-115	Sequence 115, App
c	225	24	1.7	638	3	US-09-328-111-847	Sequence 847, App
c	226	24	1.7	685	4	US-09-227-357-66	Sequence 66, Appl
c	227	24	1.7	700	1	US-08-463-115-38	Sequence 38, Appl
c	228	24	1.7	700	1	US-08-465-388-38	Sequence 38, Appl
c	229	24	1.7	703	3	US-09-313-300-6	Sequence 6, Appli
	230	24	1.7	704	3	US-09-122-400B-8	Sequence 8, Appli
	231	24	1.7	719	1	US-08-375-346A-1	Sequence 1, Appli
	232	24	1.7	719	2	US-08-467-123B-1	Sequence 1, Appli
	233	24	1.7	728	4	US-09-091-097-5	Sequence 5, Appli
	234	24	1.7	735	3	US-08-950-720A-5	Sequence 5, Appli
	235	24	1.7	764	4	US-09-288-143-57	Sequence 57, Appl
c	236	24	1.7	770	3	US-09-385-982-542	Sequence 542, App
	237	24	1.7	775	4	US-09-227-357-108	Sequence 108, App
	238	24	1.7	779	1	US-07-841-646-22	Sequence 22, Appl
	239	24	1.7	779	1	US-08-147-023-22	Sequence 22, Appl
	240	24	1.7	779	1	US-08-447-570-22	Sequence 22, Appl
	241	24	1.7	779	2	US-08-449-700-22	Sequence 22, Appl
	242	24	1.7	779	2	US-08-449-699A-22	Sequence 22, Appl
	243	24	1.7	779	4	US-09-148-925C-22	Sequence 22, Appl
	244	24	1.7	779	4	US-08-957-425-22	Sequence 22, Appl
c	245	24	1.7	780	4	US-09-328-475C-153	Sequence 153, App
	246	24	1.7	790	3	US-09-363-970-4	Sequence 4, Appli

	247	24	1.7	807	2	US-08-531-927B-9	Sequence 9, Appli
	248	24	1.7	812	4	US-09-091-097-7	Sequence 7, Appli
	249	24	1.7	818	4	US-09-366-887A-15	Sequence 15, Appl
	250	24	1.7	819	4	US-09-288-143-18	Sequence 18, Appl
	251	24	1.7	826	4	US-09-227-357-102	Sequence 102, App
	252	24	1.7	830	4	US-09-227-357-64	Sequence 64, Appl
	253	24	1.7	830	4	US-09-227-357-147	Sequence 147, App
	254	24	1.7	831	4	US-09-904-615-25	Sequence 25, Appl
	255	24	1.7	836	3	US-09-352-990-7	Sequence 7, Appli
	256	24	1.7	848	4	US-09-370-838-160	Sequence 160, App
	257	24	1.7	851	4	US-09-443-184-39	Sequence 39, Appl
	258	24	1.7	865	4	US-09-227-357-148	Sequence 148, App
c	259	24	1.7	867	4	US-09-227-357-65	Sequence 65, Appl
	260	24	1.7	902	3	US-08-924-747-5	Sequence 5, Appli
	261	24	1.7	902	3	US-09-247-373B-5	Sequence 5, Appli
	262	24	1.7	902	3	US-09-296-715-5	Sequence 5, Appli
	263	24	1.7	903	3	US-08-944-604-15	Sequence 15, Appl
	264	24	1.7	931	4	US-09-482-273-31	Sequence 31, Appl
	265	24	1.7	940	2	US-08-713-000-3	Sequence 3, Appli
	266	24	1.7	940	2	US-08-975-316-3	Sequence 3, Appli
	267	24	1.7	940	3	US-09-211-710-3	Sequence 3, Appli
	268	24	1.7	940	4	US-09-615-192A-3	Sequence 3, Appli
	269	24	1.7	944	4	US-09-227-357-122	Sequence 122, App
	270	24	1.7	955	4	US-09-641-638-11	Sequence 11, Appl
	271	24	1.7	955	4	US-09-641-638-12	Sequence 12, Appl
c	272	24	1.7	957	4	US-09-328-475C-12	Sequence 12, Appl
	273	24	1.7	985	4	US-09-220-132-154	Sequence 154, App
	274	24	1.7	991	4	US-09-369-247-52	Sequence 52, Appl
	275	24	1.7	994	4	US-09-205-258-122	Sequence 122, App
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	277	24	1.7	1001	2	US-08-473-486-10	Sequence 10, Appl
	278	24	1.7	1001	4	US-09-641-638-360	Sequence 360, App
	279	24	1.7	1001	4	US-09-641-638-361	Sequence 361, App
	280	24	1.7	1001	4	US-09-641-638-362	Sequence 362, App
	281	24	1.7	1001	4	US-09-671-317-28	Sequence 28, Appl
	282	24	1.7	1001	4	US-09-671-317-230	Sequence 230, App
	283	24	1.7	1001	4	US-09-671-317-231	Sequence 231, App
	284	24	1.7	1001	4	US-09-671-317-269	Sequence 269, App
	285	24	1.7	1013	1	US-07-920-519-30	Sequence 30, Appl
	286	24	1.7	1013	1	US-08-086-410-23	Sequence 23, Appl
	287	24	1.7	1013	1	US-08-314-586-30	Sequence 30, Appl
c	288	24	1.7	1021	4	US-09-461-325-92	Sequence 92, Appl
	289	24	1.7	1023	4	US-09-229-947-38	Sequence 38, Appl
c	290	24	1.7	1024	4	US-09-328-475C-22	Sequence 22, Appl
c	291	24	1.7	1024	4	US-09-328-475C-26	Sequence 26, Appl
	292	24	1.7	1027	4	US-09-674-741-9	Sequence 9, Appli
	293	24	1.7	1032	4	US-09-257-179-21	Sequence 21, Appl
	294	24	1.7	1040	4	US-08-978-289-5	Sequence 5, Appli
	295	24	1.7	1042	4	US-08-978-289-7	Sequence 7, Appli
	296	24	1.7	1048	4	US-09-489-847-38	Sequence 38, Appl
	297	24	1.7	1051	3	US-09-245-041-10	Sequence 10, Appl
	298	24	1.7	1053	4	US-09-257-179-31	Sequence 31, Appl
	299	24	1.7	1069	4	US-09-372-422A-7	Sequence 7, Appli
	300	24	1.7	1071	4	US-09-205-258-118	Sequence 118, App
c	301	24	1.7	1079	4	US-08-705-477E-98	Sequence 98, Appl
	302	24	1.7	1096	3	US-09-461-697-26	Sequence 26, Appl
	303	24	1.7	1100	4	US-09-372-422A-47	Sequence 47, Appl
c	304	24	1.7	1105	2	US-08-394-152A-46	Sequence 46, Appl
	305	24	1.7	1106	3	US-09-362-318-1	Sequence 1, Appli
	306	24	1.7	1118	4	US-09-522-714-23	Sequence 23, Appl
	307	24	1.7	1132	3	US-08-894-731-3	Sequence 3, Appli
	308	24	1.7	1149	4	US-09-227-357-84	Sequence 84, Appl
	309	24	1.7	1153	4	US-09-372-448A-5	Sequence 5, Appli
	310	24	1.7	1166	5	PCT-US96-12129B-1	Sequence 1, Appli
	311	24	1.7	1193	4	US-09-372-422A-23	Sequence 23, Appl
	312	24	1.7	1196	4	US-09-399-588-3	Sequence 3, Appli
	313	24	1.7	1198	3	US-09-248-335-27	Sequence 27, Appl
	314	24	1.7	1230	4	US-09-461-325-80	Sequence 80, Appl
	315	24	1.7	1238	4	US-09-369-247-50	Sequence 50, Appl
	316	24	1.7	1243	1	US-08-178-606-1	Sequence 1, Appli
	317	24	1.7	1245	3	US-09-282-305-15	Sequence 15, Appl
	318	24	1.7	1245	4	US-09-883-720-15	Sequence 15, Appl
	319	24	1.7	1265	1	US-08-182-060A-5	Sequence 5, Appli
	320	24	1.7	1265	1	US-08-712-702A-5	Sequence 5, Appli
	321	24	1.7	1279	3	US-09-277-716-31	Sequence 31, Appl
	322	24	1.7	1279	4	US-09-609-161B-31	Sequence 31, Appl
	323	24	1.7	1283	3	US-09-282-305-11	Sequence 11, Appl
	324	24	1.7	1283	4	US-09-883-720-11	Sequence 11, Appl
	325	24	1.7	1291	4	US-09-904-615-17	Sequence 17, Appl
	326	24	1.7	1292	4	US-09-904-615-61	Sequence 61, Appl
	327	24	1.7	1310	4	US-09-690-454-12	Sequence 12, Appl
	328	24	1.7	1315	3	US-09-164-193-1	Sequence 1, Appli
	329	24	1.7	1315	4	US-09-221-448A-1	Sequence 1, Appli
	330	24	1.7	1326	2	US-08-671-320-12	Sequence 12, Appl
	331	24	1.7	1326	2	US-08-868-577-12	Sequence 12, Appl
	332	24	1.7	1326	4	US-09-207-914-12	Sequence 12, Appl
	333	24	1.7	1332	2	US-09-057-762-1	Sequence 1, Appli
	334	24	1.7	1332	3	US-08-326-119A-1	Sequence 1, Appli
	335	24	1.7	1332	4	US-09-584-568C-1	Sequence 1, Appli
	336	24	1.7	1333	4	US-09-372-422A-9	Sequence 9, Appli
	337	24	1.7	1350	4	US-09-149-476-248	Sequence 248, App
	338	24	1.7	1355	4	US-09-599-360B-64	Sequence 64, Appl
	339	24	1.7	1361	4	US-09-489-847-64	Sequence 64, Appl
	340	24	1.7	1365	4	US-09-496-005-2	Sequence 2, Appli
c	341	24	1.7	1369	4	US-09-205-258-174	Sequence 174, App
	342	24	1.7	1373	3	US-08-725-758A-1	Sequence 1, Appli
	343	24	1.7	1374	1	US-08-123-761A-2	Sequence 2, Appli
	344	24	1.7	1375	4	US-09-372-422A-37	Sequence 37, Appl
	345	24	1.7	1375	4	US-09-489-847-120	Sequence 120, App
	346	24	1.7	1376	4	US-09-489-847-66	Sequence 66, Appl
	347	24	1.7	1384	4	US-09-227-357-142	Sequence 142, App
	348	24	1.7	1389	4	US-09-122-315C-9	Sequence 9, Appli
	349	24	1.7	1389	4	US-09-360-376-9	Sequence 9, Appli
	350	24	1.7	1400	4	US-09-245-281-40	Sequence 40, Appl
	351	24	1.7	1400	4	US-09-207-359B-40	Sequence 40, Appl
	352	24	1.7	1400	4	US-09-340-620A-40	Sequence 40, Appl
	353	24	1.7	1411	3	US-08-964-127-5	Sequence 5, Appli
	354	24	1.7	1411	4	US-09-496-692-5	Sequence 5, Appli
	355	24	1.7	1411	4	US-09-904-615-38	Sequence 38, Appl
	356	24	1.7	1411	4	US-10-000-273-5	Sequence 5, Appli
	357	24	1.7	1416	4	US-09-205-258-98	Sequence 98, Appl
	358	24	1.7	1428	3	US-09-118-442-5	Sequence 5, Appli
	359	24	1.7	1428	3	US-09-677-064-5	Sequence 5, Appli
	360	24	1.7	1454	4	US-09-372-422A-19	Sequence 19, Appl
	361	24	1.7	1458	4	US-09-482-273-14	Sequence 14, Appl
	362	24	1.7	1461	3	US-08-722-126A-4	Sequence 4, Appli
	363	24	1.7	1461	5	PCT-US95-04258-4	Sequence 4, Appli
	364	24	1.7	1465	4	US-09-573-906-1	Sequence 1, Appli
	365	24	1.7	1485	4	US-09-372-422A-39	Sequence 39, Appl
	366	24	1.7	1487	4	US-09-461-325-109	Sequence 109, App
	367	24	1.7	1502	2	US-08-651-940-1	Sequence 1, Appli
	368	24	1.7	1502	4	US-09-295-029-1	Sequence 1, Appli
	369	24	1.7	1505	2	US-08-909-965C-13	Sequence 13, Appl
	370	24	1.7	1508	4	US-09-039-046-1	Sequence 1, Appli
	371	24	1.7	1537	4	US-09-149-476-311	Sequence 311, App
c	372	24	1.7	1539	4	US-09-461-325-50	Sequence 50, Appl
	373	24	1.7	1540	3	US-08-977-001-2	Sequence 2, Appli
	374	24	1.7	1578	3	US-09-416-050A-1	Sequence 1, Appli
	375	24	1.7	1578	3	US-09-664-800-1	Sequence 1, Appli
	376	24	1.7	1578	3	US-09-665-309-1	Sequence 1, Appli
	377	24	1.7	1578	3	US-09-661-569-1	Sequence 1, Appli
	378	24	1.7	1599	1	US-08-143-219-27	Sequence 27, Appl
	379	24	1.7	1620	3	US-08-985-950-11	Sequence 11, Appl
	380	24	1.7	1620	4	US-09-546-049-11	Sequence 11, Appl
c	381	24	1.7	1624	2	US-08-852-807-10	Sequence 10, Appl
	382	24	1.7	1631	4	US-09-051-239A-1	Sequence 1, Appli
	383	24	1.7	1651	4	US-09-465-558-49	Sequence 49, Appl
c	384	24	1.7	1653	4	US-09-220-132-172	Sequence 172, App
	385	24	1.7	1659	1	US-08-333-358-7	Sequence 7, Appli
	386	24	1.7	1659	1	US-08-463-694-7	Sequence 7, Appli
	387	24	1.7	1659	1	US-08-694-501-7	Sequence 7, Appli
	388	24	1.7	1659	4	US-09-615-192A-124	Sequence 124, App
	389	24	1.7	1661	4	US-09-436-521A-1	Sequence 1, Appli
	390	24	1.7	1663	4	US-09-464-535-43	Sequence 43, Appl
	391	24	1.7	1664	1	US-07-863-169A-6	Sequence 6, Appli
c	392	24	1.7	1664	1	US-08-250-740-34	Sequence 34, Appl

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394	24	1.7	1664	2	US-08-429-964-6	Sequence 6, Appli
395	24	1.7	1664	3	US-07-935-087-6	Sequence 6, Appli
c 396	24	1.7	1664	4	US-09-106-375-3	Sequence 3, Appli
397	24	1.7	1664	5	PCT-US93-08062-6	Sequence 6, Appli
c 398	24	1.7	1670	3	US-08-709-838-1	Sequence 1, Appli
c 399	24	1.7	1670	3	US-08-829-839-1	Sequence 1, Appli
400	24	1.7	1674	4	US-09-482-273-78	Sequence 78, Appl
c 401	24	1.7	1681	4	US-09-461-325-115	Sequence 115, App
402	24	1.7	1689	4	US-09-053-374A-4	Sequence 4, Appli
403	24	1.7	1693	6	5169835-3	Patent No. 5169835
404	24	1.7	1697	4	US-09-345-473E-7	Sequence 7, Appli
405	24	1.7	1700	2	US-08-897-340-4	Sequence 4, Appli
406	24	1.7	1700	3	US-09-252-329-4	Sequence 4, Appli
407	24	1.7	1702	3	US-09-413-574-3	Sequence 3, Appli
408	24	1.7	1708	4	US-09-461-325-108	Sequence 108, App
409	24	1.7	1722	4	US-09-482-273-102	Sequence 102, App
410	24	1.7	1723	4	US-09-461-325-98	Sequence 98, Appl
411	24	1.7	1728	3	US-08-985-950-7	Sequence 7, Appli
412	24	1.7	1728	4	US-09-546-049-7	Sequence 7, Appli
413	24	1.7	1733	3	US-09-073-569-1	Sequence 1, Appli
414	24	1.7	1734	4	US-08-630-915A-23	Sequence 23, Appl
415	24	1.7	1753	4	US-09-149-476-56	Sequence 56, Appl
416	24	1.7	1776	2	US-08-531-927B-1	Sequence 1, Appli
417	24	1.7	1776	3	US-09-041-886-12	Sequence 12, Appl
418	24	1.7	1776	4	US-09-149-476-59	Sequence 59, Appl
419	24	1.7	1785	2	US-08-975-316-48	Sequence 48, Appl
420	24	1.7	1785	4	US-09-615-192A-48	Sequence 48, Appl
421	24	1.7	1787	4	US-09-461-325-35	Sequence 35, Appl
422	24	1.7	1796	4	US-09-470-175-1	Sequence 1, Appli
423	24	1.7	1799	3	US-09-329-633A-1	Sequence 1, Appli
424	24	1.7	1799	4	US-09-079-029-2	Sequence 2, Appli
425	24	1.7	1810	4	US-09-369-247-11	Sequence 11, Appl
426	24	1.7	1813	5	PCT-US94-12883-3	Sequence 3, Appli
427	24	1.7	1825	3	US-09-461-697-75	Sequence 75, Appl
428	24	1.7	1831	4	US-09-336-536-15	Sequence 15, Appl
429	24	1.7	1858	4	US-09-336-536-56	Sequence 56, Appl
430	24	1.7	1880	4	US-09-564-808-1	Sequence 1, Appli
431	24	1.7	1895	2	US-08-967-101-165	Sequence 165, App
432	24	1.7	1895	2	US-08-592-541-165	Sequence 165, App
433	24	1.7	1895	3	US-08-888-077A-20	Sequence 20, Appl
434	24	1.7	1895	3	US-09-124-698-165	Sequence 165, App
435	24	1.7	1895	3	US-09-127-480-165	Sequence 165, App
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445	24	1.7	1949	4	US-09-461-325-26	Sequence 26, Appl
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453	24	1.7	2000	4	US-09-439-313-374	Sequence 374, App
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466	24	1.7	2047	4	US-09-832-312-1	Sequence 1, Appli
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473	24	1.7	2119	2	US-08-381-691-17	Sequence 17, Appl
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477	24	1.7	2203	4	US-09-801-861-1	Sequence 1, Appli
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c 697	23	1.6	41	3	US-08-906-156A-89	Sequence 89, Appl
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c 699	23	1.6	41	4	US-09-920-581-9	Sequence 9, Appli
c 700	23	1.6	42	1	US-07-875-167-2	Sequence 2, Appli
c 701	23	1.6	42	1	US-08-287-164-2	Sequence 2, Appli
702	23	1.6	43	2	US-08-975-902-17	Sequence 17, Appl
703	23	1.6	43	3	US-09-251-565-17	Sequence 17, Appl
c 704	23	1.6	43	4	US-09-165-239A-5	Sequence 5, Appli
705	23	1.6	44	1	US-08-113-646A-40	Sequence 40, Appl
c 706	23	1.6	47	2	US-08-778-494B-114	Sequence 114, App
707	23	1.6	47	3	US-09-338-907-198	Sequence 198, App
708	23	1.6	47	3	US-09-338-907-275	Sequence 275, App
709	23	1.6	47	4	US-09-218-207-198	Sequence 198, App
710	23	1.6	47	4	US-09-218-207-275	Sequence 275, App
711	23	1.6	47	4	US-09-453-190B-12	Sequence 12, Appl
712	23	1.6	47	4	US-09-619-103-10	Sequence 10, Appl
c 713	23	1.6	48	1	US-08-741-881-21	Sequence 21, Appl
c 714	23	1.6	48	1	US-08-739-158-21	Sequence 21, Appl
c 715	23	1.6	48	2	US-08-739-167-21	Sequence 21, Appl
c 716	23	1.6	48	3	US-08-404-796-21	Sequence 21, Appl
c 717	23	1.6	48	3	US-08-931-869-21	Sequence 21, Appl
c 718	23	1.6	48	4	US-09-350-399-21	Sequence 21, Appl
c 719	23	1.6	48	4	US-09-236-140A-21	Sequence 21, Appl
c 720	23	1.6	50	1	US-08-233-609-5	Sequence 5, Appli
c 721	23	1.6	50	1	US-08-381-572-20	Sequence 20, Appl
c 722	23	1.6	50	1	US-08-444-083-5	Sequence 5, Appli
c 723	23	1.6	50	1	US-08-286-304-5	Sequence 5, Appli
c 724	23	1.6	50	1	US-08-442-745-5	Sequence 5, Appli
c 725	23	1.6	50	1	US-08-443-129-5	Sequence 5, Appli
c 726	23	1.6	50	1	US-08-443-952-5	Sequence 5, Appli
c 727	23	1.6	50	1	US-08-443-130-5	Sequence 5, Appli
c 728	23	1.6	50	1	US-08-592-820-20	Sequence 20, Appl
c 729	23	1.6	50	2	US-08-663-823B-72	Sequence 72, Appl
c 730	23	1.6	50	3	US-08-898-911-5	Sequence 5, Appli
c 731	23	1.6	50	5	PCT-US95-04467-5	Sequence 5, Appli
c 732	23	1.6	51	2	US-08-582-562A-8	Sequence 8, Appli
c 733	23	1.6	51	2	US-08-778-494B-8	Sequence 8, Appli
c 734	23	1.6	51	2	US-08-859-998-1373	Sequence 1373, Ap
c 735	23	1.6	51	4	US-09-225-928-1373	Sequence 1373, Ap
c 736	23	1.6	51	4	US-09-225-201B-1373	Sequence 1373, Ap
c 737	23	1.6	52	2	US-08-778-494B-111	Sequence 111, App
c 738	23	1.6	52	3	US-08-618-100B-9	Sequence 9, Appli
739	23	1.6	54	2	US-08-771-624B-24	Sequence 24, Appl
740	23	1.6	55	1	US-08-113-646A-41	Sequence 41, Appl
c 741	23	1.6	55	2	US-08-522-269B-18	Sequence 18, Appl
c 742	23	1.6	55	2	US-08-582-562A-16	Sequence 16, Appl
c 743	23	1.6	55	2	US-08-778-494B-16	Sequence 16, Appl
c 744	23	1.6	55	2	US-08-778-494B-67	Sequence 67, Appl
c 745	23	1.6	55	3	US-09-294-923-18	Sequence 18, Appl
746	23	1.6	55	4	US-09-944-036-32	Sequence 32, Appl
747	23	1.6	56	3	US-09-118-256-1	Sequence 1, Appli
c 748	23	1.6	56	3	US-09-118-256-2	Sequence 2, Appli
749	23	1.6	56	4	US-09-944-036-30	Sequence 30, Appl
750	23	1.6	57	3	US-09-620-958A-7	Sequence 7, Appli
751	23	1.6	57	4	US-09-944-036-31	Sequence 31, Appl
c 752	23	1.6	58	2	US-08-778-494B-109	Sequence 109, App
c 753	23	1.6	59	2	US-08-778-494B-110	Sequence 110, App
c 754	23	1.6	60	1	US-08-241-465B-11	Sequence 11, Appl
c 755	23	1.6	60	4	US-09-499-362-1	Sequence 1, Appli
c 756	23	1.6	60	4	US-09-284-627-14	Sequence 14, Appl
757	23	1.6	61	4	US-09-457-959-7	Sequence 7, Appli
758	23	1.6	64	1	US-08-055-390-10	Sequence 10, Appl
c 759	23	1.6	65	4	US-09-415-784-32	Sequence 32, Appl
c 760	23	1.6	65	4	US-09-415-785A-32	Sequence 32, Appl
c 761	23	1.6	65	4	US-08-944-465-32	Sequence 32, Appl
c 762	23	1.6	65	4	US-09-415-868-32	Sequence 32, Appl
c 763	23	1.6	65	4	US-09-415-900-32	Sequence 32, Appl
c 764	23	1.6	66	4	US-09-183-636-1	Sequence 1, Appli
c 765	23	1.6	67	2	US-08-972-225-1	Sequence 1, Appli
c 766	23	1.6	67	3	US-09-337-944-1	Sequence 1, Appli
767	23	1.6	67	3	US-09-620-958A-6	Sequence 6, Appli
c 768	23	1.6	80	4	US-09-284-627-15	Sequence 15, Appl
c 769	23	1.6	90	3	US-09-065-058-16	Sequence 16, Appl
c 770	23	1.6	91	4	US-09-404-879A-201	Sequence 201, App
c 771	23	1.6	91	4	US-09-338-933-201	Sequence 201, App
c 772	23	1.6	91	4	US-09-215-681-201	Sequence 201, App
773	23	1.6	92	1	US-08-120-827-94	Sequence 94, Appl
774	23	1.6	92	1	US-08-478-675-94	Sequence 94, Appl
c 775	23	1.6	100	3	US-08-991-789A-30	Sequence 30, Appl
c 776	23	1.6	100	4	US-09-062-451-30	Sequence 30, Appl
c 777	23	1.6	100	4	US-09-598-326-30	Sequence 30, Appl
c 778	23	1.6	100	4	US-09-289-198-30	Sequence 30, Appl
c 779	23	1.6	101	4	US-09-404-879A-293	Sequence 293, App
c 780	23	1.6	101	4	US-09-338-933-293	Sequence 293, App
c 781	23	1.6	101	4	US-09-215-681-293	Sequence 293, App
782	23	1.6	105	3	US-08-746-111-37	Sequence 37, Appl
c 783	23	1.6	105	4	US-09-284-627-23	Sequence 23, Appl
784	23	1.6	109	1	US-08-120-827-82	Sequence 82, Appl
785	23	1.6	109	1	US-08-478-675-82	Sequence 82, Appl
c 786	23	1.6	113	4	US-09-367-927A-1	Sequence 1, Appli
787	23	1.6	114	1	US-08-120-827-99	Sequence 99, Appl
788	23	1.6	114	1	US-08-478-675-99	Sequence 99, Appl
789	23	1.6	120	1	US-08-153-051B-28	Sequence 28, Appl
790	23	1.6	120	1	US-08-060-952C-44	Sequence 44, Appl
791	23	1.6	120	2	US-08-151-477A-28	Sequence 28, Appl
792	23	1.6	120	3	US-08-819-867-58	Sequence 58, Appl
793	23	1.6	120	4	US-08-464-011B-44	Sequence 44, Appl
794	23	1.6	120	4	US-09-378-535-58	Sequence 58, Appl
c 795	23	1.6	128	4	US-09-183-266A-10	Sequence 10, Appl
c 796	23	1.6	130	6	5198345-15	Patent No. 5198345
c 797	23	1.6	132	4	US-09-702-705-1074	Sequence 1074, Ap
c 798	23	1.6	132	4	US-09-736-457-1074	Sequence 1074, Ap
c 799	23	1.6	141	3	US-08-737-078A-1	Sequence 1, Appli
c 800	23	1.6	141	5	PCT-US94-04706-1	Sequence 1, Appli
801	23	1.6	144	1	US-08-702-344-26	Sequence 26, Appl
802	23	1.6	144	4	US-09-702-705-776	Sequence 776, App
803	23	1.6	144	4	US-09-736-457-776	Sequence 776, App
804	23	1.6	165	2	US-08-783-395-3	Sequence 3, Appli
805	23	1.6	165	2	US-08-924-838-9	Sequence 9, Appli
c 806	23	1.6	193	3	US-08-991-789A-266	Sequence 266, App
c 807	23	1.6	193	4	US-09-062-451-266	Sequence 266, App
c 808	23	1.6	193	4	US-09-289-198-266	Sequence 266, App
c 809	23	1.6	199	4	US-09-222-575-125	Sequence 125, App
c 810	23	1.6	199	4	US-09-389-681-125	Sequence 125, App
c 811	23	1.6	199	4	US-09-620-405B-125	Sequence 125, App
c 812	23	1.6	199	4	US-09-339-338-125	Sequence 125, App
c 813	23	1.6	199	4	US-09-433-826B-125	Sequence 125, App
c 814	23	1.6	199	4	US-09-604-287A-125	Sequence 125, App
815	23	1.6	208	1	US-08-686-878A-37	Sequence 37, Appl
c 816	23	1.6	208	2	US-08-967-101-98	Sequence 98, Appl
c 817	23	1.6	208	2	US-08-592-541-98	Sequence 98, Appl
c 818	23	1.6	208	3	US-09-124-698-98	Sequence 98, Appl
c 819	23	1.6	208	3	US-09-127-480-98	Sequence 98, Appl
c 820	23	1.6	208	3	US-08-496-841C-98	Sequence 98, Appl
821	23	1.6	208	4	US-09-175-928-37	Sequence 37, Appl
c 822	23	1.6	208	4	US-09-124-523-98	Sequence 98, Appl
c 823	23	1.6	208	4	US-09-636-796A-98	Sequence 98, Appl
c 824	23	1.6	208	4	US-08-431-048F-98	Sequence 98, Appl
825	23	1.6	222	3	US-08-481-190-15	Sequence 15, Appl
826	23	1.6	222	5	PCT-US93-00869-15	Sequence 15, Appl
827	23	1.6	223	4	US-09-792-594-11	Sequence 11, Appl
c 828	23	1.6	224	2	US-08-731-272A-26	Sequence 26, Appl
829	23	1.6	228	3	US-09-328-111-484	Sequence 484, App
c 830	23	1.6	231	3	US-09-328-111-287	Sequence 287, App

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c	832	23	1.6	241	4	US-09-389-681-333	Sequence 333, App
	833	23	1.6	241	4	US-09-389-681-334	Sequence 334, App
c	834	23	1.6	241	4	US-09-620-405B-333	Sequence 333, App
	835	23	1.6	241	4	US-09-620-405B-334	Sequence 334, App
c	836	23	1.6	241	4	US-09-433-826B-333	Sequence 333, App
	837	23	1.6	241	4	US-09-433-826B-334	Sequence 334, App
c	838	23	1.6	241	4	US-09-604-287A-333	Sequence 333, App
	839	23	1.6	241	4	US-09-604-287A-334	Sequence 334, App
	840	23	1.6	245	4	US-09-149-476-70	Sequence 70, Appl
	841	23	1.6	247	1	US-08-691-641-4	Sequence 4, Appli
c	842	23	1.6	257	3	US-09-385-982-370	Sequence 370, App
c	843	23	1.6	271	2	US-08-731-272A-29	Sequence 29, Appl
	844	23	1.6	275	3	US-09-328-111-385	Sequence 385, App
	845	23	1.6	277	3	US-09-007-005-3	Sequence 3, Appli
	846	23	1.6	277	3	US-09-244-796-3	Sequence 3, Appli
	847	23	1.6	278	4	US-09-370-838-159	Sequence 159, App
	848	23	1.6	289	1	US-08-341-568-3	Sequence 3, Appli
	849	23	1.6	289	2	US-08-911-020-3	Sequence 3, Appli
	850	23	1.6	289	3	US-09-007-005-17	Sequence 17, Appl
	851	23	1.6	289	3	US-09-244-796-17	Sequence 17, Appl
c	852	23	1.6	296	2	US-09-032-684-13	Sequence 13, Appl
c	853	23	1.6	296	3	US-09-385-982-19	Sequence 19, Appl
	854	23	1.6	300	4	US-09-205-258-143	Sequence 143, App
c	855	23	1.6	302	4	US-09-439-313-255	Sequence 255, App
c	856	23	1.6	302	4	US-09-352-616A-255	Sequence 255, App
c	857	23	1.6	302	4	US-09-232-149A-255	Sequence 255, App
	858	23	1.6	309	1	US-08-086-410-24	Sequence 24, Appl
	859	23	1.6	319	2	US-08-244-537-11	Sequence 11, Appl
c	860	23	1.6	321	3	US-09-385-982-366	Sequence 366, App
c	861	23	1.6	322	3	US-09-385-982-216	Sequence 216, App
c	862	23	1.6	322	3	US-09-385-982-362	Sequence 362, App
	863	23	1.6	324	2	US-08-721-925A-4	Sequence 4, Appli
c	864	23	1.6	327	3	US-09-385-982-544	Sequence 544, App
c	865	23	1.6	333	3	US-09-328-111-797	Sequence 797, App
	866	23	1.6	336	3	US-09-385-982-508	Sequence 508, App
c	867	23	1.6	337	3	US-09-328-111-586	Sequence 586, App
c	868	23	1.6	340	1	US-08-171-385-27	Sequence 27, Appl
c	869	23	1.6	340	3	US-08-361-441B-27	Sequence 27, Appl
	870	23	1.6	340	3	US-09-385-982-394	Sequence 394, App
c	871	23	1.6	342	3	US-09-385-982-342	Sequence 342, App
	872	23	1.6	347	1	US-08-104-072B-2	Sequence 2, Appli
c	873	23	1.6	348	3	US-09-385-982-283	Sequence 283, App
c	874	23	1.6	349	3	US-09-385-982-22	Sequence 22, Appl
c	875	23	1.6	350	1	US-08-171-385-14	Sequence 14, Appl
	876	23	1.6	350	1	US-08-248-016-11	Sequence 11, Appl
	877	23	1.6	350	1	US-08-276-452A-48	Sequence 48, Appl
	878	23	1.6	350	1	US-08-451-501-11	Sequence 11, Appl
	879	23	1.6	350	2	US-08-798-744-48	Sequence 48, Appl
c	880	23	1.6	350	3	US-08-361-441B-14	Sequence 14, Appl
	881	23	1.6	350	5	PCT-US95-06761-11	Sequence 11, Appl
	882	23	1.6	360	1	US-07-920-519-28	Sequence 28, Appl
	883	23	1.6	360	1	US-08-086-410-21	Sequence 21, Appl
	884	23	1.6	360	1	US-08-314-586-28	Sequence 28, Appl
c	885	23	1.6	361	3	US-09-385-982-26	Sequence 26, Appl
	886	23	1.6	367	3	US-09-328-111-446	Sequence 446, App
	887	23	1.6	370	4	US-09-376-113-1	Sequence 1, Appli
c	888	23	1.6	374	3	US-09-385-982-135	Sequence 135, App
	889	23	1.6	375	3	US-08-946-026-23	Sequence 23, Appl
c	890	23	1.6	376	4	US-09-220-132-128	Sequence 128, App
	891	23	1.6	380	1	US-08-126-587C-5	Sequence 5, Appli
c	892	23	1.6	390	3	US-09-385-982-232	Sequence 232, App
c	893	23	1.6	390	4	US-09-222-575-90	Sequence 90, Appl
c	894	23	1.6	390	4	US-09-389-681-90	Sequence 90, Appl
c	895	23	1.6	390	4	US-09-620-405B-90	Sequence 90, Appl
c	896	23	1.6	390	4	US-09-339-338-90	Sequence 90, Appl
c	897	23	1.6	390	4	US-09-433-826B-90	Sequence 90, Appl
c	898	23	1.6	390	4	US-09-604-287A-90	Sequence 90, Appl
c	899	23	1.6	393	4	US-09-439-313-357	Sequence 357, App
c	900	23	1.6	393	4	US-09-352-616A-357	Sequence 357, App
	901	23	1.6	396	2	US-08-630-822A-84	Sequence 84, Appl
	902	23	1.6	396	2	US-09-005-069-84	Sequence 84, Appl
	903	23	1.6	396	4	US-09-171-156A-33	Sequence 33, Appl
	904	23	1.6	396	4	US-09-004-730A-33	Sequence 33, Appl
	905	23	1.6	396	4	US-08-981-799A-33	Sequence 33, Appl
	906	23	1.6	398	4	US-09-904-615-62	Sequence 62, Appl
	907	23	1.6	399	1	US-07-885-970A-13	Sequence 13, Appl
	908	23	1.6	399	1	US-08-298-687A-13	Sequence 13, Appl
c	909	23	1.6	399	1	US-08-530-797-12	Sequence 12, Appl
	910	23	1.6	399	1	US-08-298-829-13	Sequence 13, Appl
c	911	23	1.6	399	2	US-08-787-335-12	Sequence 12, Appl
c	912	23	1.6	403	3	US-09-385-982-29	Sequence 29, Appl
c	913	23	1.6	403	4	US-09-387-212-2	Sequence 2, Appli
c	914	23	1.6	403	4	US-09-948-802-2	Sequence 2, Appli
c	915	23	1.6	408	4	US-09-222-575-43	Sequence 43, Appl
c	916	23	1.6	408	4	US-09-389-681-43	Sequence 43, Appl
c	917	23	1.6	408	4	US-09-620-405B-43	Sequence 43, Appl
c	918	23	1.6	408	4	US-09-339-338-43	Sequence 43, Appl
c	919	23	1.6	408	4	US-09-433-826B-43	Sequence 43, Appl
c	920	23	1.6	408	4	US-09-604-287A-43	Sequence 43, Appl
c	921	23	1.6	412	4	US-09-702-705-1047	Sequence 1047, Ap
c	922	23	1.6	412	4	US-09-736-457-1047	Sequence 1047, Ap
	923	23	1.6	413	2	US-09-014-969-5	Sequence 5, Appli
c	924	23	1.6	413	3	US-09-328-111-25	Sequence 25, Appl
	925	23	1.6	427	4	US-09-091-097-41	Sequence 41, Appl
c	926	23	1.6	435	3	US-09-385-982-518	Sequence 518, App
c	927	23	1.6	436	4	US-09-439-313-353	Sequence 353, App
c	928	23	1.6	436	4	US-09-352-616A-353	Sequence 353, App
	929	23	1.6	437	3	US-09-040-984-74	Sequence 74, Appl
	930	23	1.6	437	4	US-09-123-912-74	Sequence 74, Appl
	931	23	1.6	437	4	US-09-643-597-74	Sequence 74, Appl
	932	23	1.6	437	4	US-09-480-884A-74	Sequence 74, Appl
	933	23	1.6	437	4	US-09-542-615A-74	Sequence 74, Appl
	934	23	1.6	437	4	US-09-606-421B-74	Sequence 74, Appl
	935	23	1.6	444	3	US-08-688-988-44	Sequence 44, Appl
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c	937	23	1.6	450	2	US-08-592-541-7	Sequence 7, Appli
c	938	23	1.6	450	3	US-09-124-698-7	Sequence 7, Appli
c	939	23	1.6	450	3	US-09-127-480-7	Sequence 7, Appli
c	940	23	1.6	450	3	US-08-496-841C-7	Sequence 7, Appli
c	941	23	1.6	450	3	US-09-385-982-155	Sequence 155, App
c	942	23	1.6	450	4	US-09-124-523-7	Sequence 7, Appli
c	943	23	1.6	450	4	US-09-636-796A-7	Sequence 7, Appli
	944	23	1.6	450	4	US-09-702-705-388	Sequence 388, App
	945	23	1.6	450	4	US-09-736-457-388	Sequence 388, App
c	946	23	1.6	450	4	US-08-431-048F-7	Sequence 7, Appli
c	947	23	1.6	457	3	US-09-385-982-15	Sequence 15, Appl
	948	23	1.6	458	1	US-08-524-757-1	Sequence 1, Appli
	949	23	1.6	458	2	US-08-924-759-7	Sequence 7, Appli
	950	23	1.6	458	3	US-09-248-335-7	Sequence 7, Appli
	951	23	1.6	462	3	US-09-385-982-504	Sequence 504, App
	952	23	1.6	466	3	US-09-328-111-239	Sequence 239, App
c	953	23	1.6	467	4	US-09-328-475C-122	Sequence 122, App
c	954	23	1.6	469	3	US-09-328-111-436	Sequence 436, App
c	955	23	1.6	469	4	US-09-222-575-128	Sequence 128, App
c	956	23	1.6	469	4	US-09-389-681-128	Sequence 128, App
c	957	23	1.6	469	4	US-09-620-405B-128	Sequence 128, App
c	958	23	1.6	469	4	US-09-339-338-128	Sequence 128, App
c	959	23	1.6	469	4	US-09-433-826B-128	Sequence 128, App
c	960	23	1.6	469	4	US-09-604-287A-128	Sequence 128, App
	961	23	1.6	471	5	PCT-US95-13658-1	Sequence 1, Appli
	962	23	1.6	472	4	US-09-394-630-1	Sequence 1, Appli
c	963	23	1.6	472	4	US-09-702-705-892	Sequence 892, App
c	964	23	1.6	472	4	US-09-736-457-892	Sequence 892, App
	965	23	1.6	474	3	US-08-516-859A-97	Sequence 97, Appl
	966	23	1.6	474	4	US-09-586-472-97	Sequence 97, Appl
	967	23	1.6	474	4	US-09-528-706-97	Sequence 97, Appl
	968	23	1.6	476	3	US-09-020-956-80	Sequence 80, Appl
	969	23	1.6	476	3	US-09-030-607-80	Sequence 80, Appl
	970	23	1.6	476	4	US-09-439-313-80	Sequence 80, Appl
	971	23	1.6	476	4	US-09-352-616A-80	Sequence 80, Appl
	972	23	1.6	476	4	US-09-232-149A-80	Sequence 80, Appl
c	973	23	1.6	476	4	US-09-220-132-157	Sequence 157, App
c	974	23	1.6	479	3	US-09-328-111-432	Sequence 432, App
	975	23	1.6	495	4	US-09-105-542A-13	Sequence 13, Appl
c	976	23	1.6	495	4	US-09-220-132-186	Sequence 186, App

977	23	1.6	496	4	US-09-904-615-60	Sequence 60, Appl
c 978	23	1.6	502	4	US-09-186-276B-29	Sequence 29, Appl
c 979	23	1.6	502	4	US-08-842-445-29	Sequence 29, Appl
c 980	23	1.6	502	4	US-09-186-188B-29	Sequence 29, Appl
981	23	1.6	506	4	US-09-370-838-263	Sequence 263, App
982	23	1.6	519	4	US-09-227-357-76	Sequence 76, Appl
c 983	23	1.6	520	4	US-09-220-132-171	Sequence 171, App
984	23	1.6	522	2	US-08-909-965C-16	Sequence 16, Appl
985	23	1.6	528	4	US-09-105-542A-12	Sequence 12, Appl
986	23	1.6	530	4	US-09-461-325-28	Sequence 28, Appl
c 987	23	1.6	535	3	US-09-385-982-385	Sequence 385, App
c 988	23	1.6	537	4	US-09-720-201A-4	Sequence 4, Appli
989	23	1.6	540	4	US-09-313-434C-15	Sequence 15, Appl
990	23	1.6	543	4	US-09-904-615-33	Sequence 33, Appl
c 991	23	1.6	545	3	US-09-328-111-506	Sequence 506, App
c 992	23	1.6	546	4	US-09-280-116-48	Sequence 48, Appl
c 993	23	1.6	547	3	US-09-188-930-14	Sequence 14, Appl
c 994	23	1.6	547	4	US-09-312-283C-14	Sequence 14, Appl
995	23	1.6	548	4	US-09-186-276B-51	Sequence 51, Appl
996	23	1.6	548	4	US-08-842-445-51	Sequence 51, Appl
997	23	1.6	548	4	US-09-186-188B-51	Sequence 51, Appl
998	23	1.6	549	3	US-09-091-590A-13	Sequence 13, Appl
c 999	23	1.6	549	4	US-09-342-681C-6	Sequence 6, Appli
1000	23	1.6	550	3	US-08-632-511A-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT 1
US-09-220-132-133
; Sequence 133, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
;  TITLE OF INVENTION:  OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
;  FILE REFERENCE:  07334-074001
;  CURRENT APPLICATION NUMBER: US/09/220,132
;  CURRENT FILING DATE:  1998-12-23
;  PRIOR APPLICATION NUMBER:  US 60/079,303
;  PRIOR FILING DATE:  1998-03-25
;  PRIOR APPLICATION NUMBER:  US 60/068,821
;  PRIOR FILING DATE:  1997-12-24
;  NUMBER OF SEQ ID NOS:  191
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;   LENGTH: 693
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-220-132-133

  Query Match             1.9%;  Score 27;  DB 4;  Length 693;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1369 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 1395
              |||||||||||||||||||||||||||
Db        663 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 689


RESULT 2
US-09-220-132-191
; Sequence 191, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
;  TITLE OF INVENTION:  OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
;  FILE REFERENCE:  07334-074001
;  CURRENT APPLICATION NUMBER: US/09/220,132
;  CURRENT FILING DATE:  1998-12-23
;  PRIOR APPLICATION NUMBER:  US 60/079,303
;  PRIOR FILING DATE:  1998-03-25
;  PRIOR APPLICATION NUMBER:  US 60/068,821
;  PRIOR FILING DATE:  1997-12-24
;  NUMBER OF SEQ ID NOS:  191
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 191
;   LENGTH: 775
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-220-132-191

  Query Match             1.9%;  Score 27;  DB 4;  Length 775;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1369 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 1395
              |||||||||||||||||||||||||||
Db        745 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 771


RESULT 3
US-09-220-132-175
; Sequence 175, Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
;  APPLICANT:  Shyjan, Andrew W.
;  TITLE OF INVENTION:  METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
;  TITLE OF INVENTION:  OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
;  FILE REFERENCE:  07334-074001
;  CURRENT APPLICATION NUMBER: US/09/220,132
;  CURRENT FILING DATE:  1998-12-23
;  PRIOR APPLICATION NUMBER:  US 60/079,303
;  PRIOR FILING DATE:  1998-03-25
;  PRIOR APPLICATION NUMBER:  US 60/068,821
;  PRIOR FILING DATE:  1997-12-24
;  NUMBER OF SEQ ID NOS:  191
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 175
;   LENGTH: 1223
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-220-132-175

  Query Match             1.9%;  Score 27;  DB 4;  Length 1223;
  Best Local Similarity   100.0%;  Pred. No. 0.026;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1369 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 1395
              |||||||||||||||||||||||||||
Db       1193 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 1219


RESULT 4
US-08-473-981A-5
; Sequence 5, Application US/08473981A
; Patent No. 5629162
;  GENERAL INFORMATION:
;    APPLICANT:  deFougerolles, Antonin R
;    APPLICANT:  Springer, Timothy A
;    TITLE OF INVENTION:  METHODS OF IDENTIFYING AGENTS WHICH MODULATE
;    TITLE OF INVENTION:  ICAM-3 BINDING TO LFA-1 (AS AMENDED)
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, N.W. SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/473,981A
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MILLONIG, ROBERT C
;       REGISTRATION NUMBER:  34,395
;       REFERENCE/DOCKET NUMBER:  1011.0560004
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1817 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  9..1649
US-08-473-981A-5

  Query Match             1.9%;  Score 27;  DB 1;  Length 1817;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1364 TCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              |||||||||||||||||||||||||||
Db       1727 TCCCTAAAAAAAAAAAAAAAAAAAAAA 1753


RESULT 5
US-08-474-087-5
; Sequence 5, Application US/08474087
; Patent No. 5891841
;  GENERAL INFORMATION:
;     APPLICANT:  de Fougerolles, Antonin R
;     APPLICANT:  Springer, Timothy A
;     TITLE OF INVENTION:  METHODS OF USING INTERCELLULAR ADHESION MOLECULE-       3 (IC
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;       STREET:  1100 NEW YORK AVENUE, N.W. SUITE 600
;       CITY:  WASHINGTON
;       STATE:  D. C.
;       COUNTRY:  USA
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/474,087
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/038,990
;       FILING DATE:  23-DEC-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/712,879
;       FILING DATE:  11-JUN-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MILLONIG, ROBERT C
;       REGISTRATION NUMBER:  34,395
;       REFERENCE/DOCKET NUMBER:  1011.0560003
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1817 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  both
;       TOPOLOGY:  both
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  9..1649
US-08-474-087-5

  Query Match             1.9%;  Score 27;  DB 2;  Length 1817;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1364 TCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              |||||||||||||||||||||||||||
Db       1727 TCCCTAAAAAAAAAAAAAAAAAAAAAA 1753


RESULT 6
US-09-130-491-7
; Sequence 7, Application US/09130491
; Patent No. 6416974
; GENERAL INFORMATION:
;  APPLICANT: Holtzman, Douglas A.
;  APPLICANT: Goodearl, Andrew D.J.
;  TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
;  FILE REFERENCE: 09404/041001
;  CURRENT APPLICATION NUMBER: US/09/130,491
;  CURRENT FILING DATE: 1998-08-07
;  EARLIER APPLICATION NUMBER: US 60/058,108
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: US 60/054,961
;  EARLIER FILING DATE: 1997-08-06
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 2114
;   TYPE: DNA
;   ORGANISM: Rattus rattus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3)...(1445)
US-09-130-491-7

  Query Match             1.9%;  Score 27;  DB 4;  Length 2114;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1369 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 1395
              |||||||||||||||||||||||||||
Db       2084 AAAAAAAAAAAAAAAAAAAAAAAGGCGG 2110


RESULT 7
US-09-798-096-10/c
; Sequence 10, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Andrew T. Watt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL2 EXPRESSION
;  FILE REFERENCE: RTS-0207
;  CURRENT APPLICATION NUMBER: US/09/798,096
;  CURRENT FILING DATE:  2001-03-01
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
;   LENGTH: 99500
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-798-096-10
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Query Match 1.9%; Score 27; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1367 CTAAAAAAAAAAAAAAAAAAAAAAGGC 1393
||||||||||||||||||||||||||
Db 57302 CTAAAAAAAAAAAAAAAAAAAAAAGGC 57276

RESULT 8
US-09-328-475C-196/c
; Sequence 196, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; TITLE OF INVENTION: ARE DIFFERENTIALLY REGULATED IN PROSTATE CANCER
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 196
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(511)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-196

Query Match 1.9%; Score 26; DB 4; Length 511;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1365 CCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||
Db 138 CCCTAAAAAAAAAAAAAAAAAAAAAA 113

RESULT 9
US-09-122-400B-11
; Sequence 11, Application US/09122400B
; Patent No. 6245974
; GENERAL INFORMATION:
; APPLICANT: Michalowski, Susan
; APPLICANT: Spiker, Steven
; TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
; FILE REFERENCE: Michalowski and Spiker
; CURRENT APPLICATION NUMBER: US/09/122,400B
; CURRENT FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 60/066,118
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 899
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-122-400B-11

Query Match 1.9%; Score 26; DB 3; Length 899;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1365 CCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||
Db 804 CCCTAAAAAAAAAAAAAAAAAAAAAA 829

RESULT 10
US-09-257-179-28
; Sequence 28, Application US/09257179
; Patent No. 6410709
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: PZ015P1
; CURRENT APPLICATION NUMBER: US/09/257,179
; CURRENT FILING DATE: 1999-02-25
; EARLIER APPLICATION NUMBER: PCT/US98/17709
; EARLIER FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 60/056,270
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,271
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,247
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,073
; EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-257-179-28

Query Match 1.9%; Score 26; DB 4; Length 1327;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1370 AAAAAAAAAAAAAAAAAAAAAAGGCGG 1395
||||||||||||||||||||||||||
Db 1300 AAAAAAAAAAAAAAAAAAAAAAGGCGG 1325

RESULT 11
US-09-620-312D-722
; Sequence 722, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21

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;  NUMBER OF SEQ ID NOS: 1105
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 722
;    LENGTH: 1509
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (557)..(1312)
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(1509)
;    OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-722

  Query Match             1.9%;  Score 26;  DB 4;  Length 1509;
  Best Local Similarity   100.0%;  Pred. No. 0.067;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1365 CCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              ||||||||||||||||||||||||||
Db       1484 CCCTAAAAAAAAAAAAAAAAAAAAAA 1509


RESULT 12
US-09-482-273-51
; Sequence 51, Application US/09482273
; Patent No. 6534631
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 71 Human Secreted Proteins
;  FILE REFERENCE: PZ030P1
;  CURRENT APPLICATION NUMBER: US/09/482,273
;  CURRENT FILING DATE: 2000-01-13
;  EARLIER APPLICATION NUMBER: PCT/US99/15849
;  EARLIER FILING DATE: 1999-07-14
;  EARLIER APPLICATION NUMBER: 60/092,921
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/092,922
;  EARLIER FILING DATE: 1998-07-15
;  EARLIER APPLICATION NUMBER: 60/092,956
;  EARLIER FILING DATE: 1998-07-15
;  NUMBER OF SEQ ID NOS: 267
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
;    LENGTH: 1569
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (341)
;    OTHER INFORMATION: n equals a,t,g, or c
US-09-482-273-51

  Query Match             1.9%;  Score 26;  DB 4;  Length 1569;
  Best Local Similarity   100.0%;  Pred. No. 0.067;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1365 CCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              ||||||||||||||||||||||||||
Db       1537 CCCTAAAAAAAAAAAAAAAAAAAAAA 1562


RESULT 13
US-09-489-847-48
; Sequence 48, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
;    LENGTH: 1730
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-489-847-48

  Query Match             1.9%;  Score 26;  DB 4;  Length 1730;
  Best Local Similarity   100.0%;  Pred. No. 0.067;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1367 CTAAAAAAAAAAAAAAAAAAAAAAGG 1392
              ||||||||||||||||||||||||||
Db       1699 CTAAAAAAAAAAAAAAAAAAAAAAGG 1724


RESULT 14
US-08-836-567-3
; Sequence 3, Application US/08836567
; Patent No. 6130367
;  GENERAL INFORMATION:
;    APPLICANT:  Kossmann, Jens
;    APPLICANT:  Springer, Franziska
;    APPLICANT:  Abel, Gernot
;    TITLE OF INVENTION:  DNA MOLECULES THAT CODE FOR ENZYMES
;    TITLE OF INVENTION:  INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
;    TITLE OF INVENTION:  PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FISH & NEAVE
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,567
;      FILING DATE:  24-JUL-1997
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/04415
;      FILING DATE:  09-NOV-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 44 41 408.0
;      FILING DATE:  10-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr., James F.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  Agrevo-4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-596-9000
;      TELEFAX:  212-596-9090
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1758 base pairs
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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US-08-836-567-3

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; Patent No. 6483010
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;       APPLICANT: Kossmann, Jens
;                  Springer, Franziska
;                  Abel, Gernot
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;                           PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
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;            ADDRESSEE: FISH & NEAVE
;            STREET: 1251 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10020
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
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;            FILING DATE: 28-Jun-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
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;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: DE P 44 41 408.0
;            FILING DATE: 10-NOV-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Haley Jr., James F.
;            REGISTRATION NUMBER: 27,794
;            REFERENCE/DOCKET NUMBER: Agrevo-4
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;            TELEPHONE: 212-596-9000
;            TELEFAX: 212-596-9090
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;            LENGTH: 1758 base pairs
;            TYPE: nucleotide
;            STRANDEDNESS: unknown
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA to mRNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
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;            ORGANISM: Solanum tuberosum
;            STRAIN: cv. Berolina
;            TISSUE TYPE: tuber tissue
;       IMMEDIATE SOURCE:
;            LIBRARY: cDNA-library in pBluescriptSKII+
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;            LOCATION: 1..1377
;            OTHER INFORMATION: /function= "Polymerization of
;            starch"
;            /product= "Starch synthase"
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463	30	2.1	2457	15	US-10-184-624-569	Sequence 569, App
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466	30	2.1	2457	15	US-10-197-706-569	Sequence 569, App
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478	30	2.1	2457	15	US-10-187-739-569	Sequence 569, App
479	30	2.1	2457	15	US-10-206-907-569	Sequence 569, App
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c 483	29	2.1	398	15	US-10-040-862-8628	Sequence 8628, Ap
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c 485	29	2.1	4301	10	US-09-989-919-69	Sequence 69, Appl
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488	28	2.0	458	14	US-10-001-835-78	Sequence 78, Appl
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c 498	27	1.9	287	10	US-09-983-965-3686	Sequence 3686, Ap
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	537	27	1.9	1817	10	US-09-954-531-383	Sequence 383, App
	538	27	1.9	1824	15	US-10-207-655-155	Sequence 155, App
	539	27	1.9	2114	13	US-10-365-227-7	Sequence 7, Appli
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c	569	26	1.9	77	11	US-09-997-279-162	Sequence 162, App
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c	572	26	1.9	173	10	US-09-920-300A-955	Sequence 955, App
c	573	26	1.9	173	13	US-10-099-926-955	Sequence 955, App
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c	582	26	1.9	208	10	US-09-833-263-600	Sequence 600, App
	583	26	1.9	208	10	US-09-867-701-9150	Sequence 9150, Ap
c	584	26	1.9	208	14	US-10-025-380-600	Sequence 600, App
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	637	26	1.9	473	11	US-09-918-995-31158	Sequence 31158, A
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	647	26	1.9	515	13	US-10-027-632-215720	Sequence 215720,
	648	26	1.9	515	14	US-10-027-632-215720	Sequence 215720,
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	665	26	1.9	595	9	US-09-764-898-65	Sequence 65, Appl
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684	26	1.9	784	13	US-10-257-826A-205	Sequence 205, App
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686	26	1.9	875	13	US-09-814-353-21852	Sequence 21852, A
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689	26	1.9	927	14	US-10-001-887-6	Sequence 6, Appli
c 690	26	1.9	944	9	US-09-770-445-350	Sequence 350, App
691	26	1.9	981	9	US-09-782-980-22	Sequence 22, Appl
692	26	1.9	1062	15	US-10-106-698-1234	Sequence 1234, Ap
693	26	1.9	1192	15	US-10-180-375-79	Sequence 79, Appl
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695	26	1.9	1242	15	US-10-084-994-3	Sequence 3, Appli
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697	26	1.9	1318	11	US-09-866-050A-597	Sequence 597, App
698	26	1.9	1318	15	US-10-152-661-597	Sequence 597, App
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704	26	1.9	1509	15	US-10-037-270-722	Sequence 722, App
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706	26	1.9	1569	11	US-09-984-271-51	Sequence 51, Appl
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c 713	26	1.9	2123	11	US-09-956-622A-29	Sequence 29, Appl
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715	26	1.9	2269	15	US-10-074-475-128	Sequence 128, App
716	26	1.9	2362	13	US-10-220-891-48	Sequence 48, Appl
717	26	1.9	2429	14	US-10-044-090-344	Sequence 344, App
718	26	1.9	2528	10	US-09-925-300-582	Sequence 582, App
719	26	1.9	2660	9	US-09-838-561-1	Sequence 1, Appli
720	26	1.9	2660	9	US-09-816-760-1	Sequence 1, Appli
721	26	1.9	2660	13	US-10-172-585-1	Sequence 1, Appli
722	26	1.9	3149	13	US-10-007-926A-64	Sequence 64, Appl
723	26	1.9	3149	15	US-10-225-567A-89	Sequence 89, Appl
724	26	1.9	3289	9	US-09-739-254-11	Sequence 11, Appl
725	26	1.9	3289	9	US-09-904-615-11	Sequence 11, Appl
726	26	1.9	3289	13	US-10-055-098-11	Sequence 11, Appl
727	26	1.9	3289	15	US-10-054-988-11	Sequence 11, Appl
728	26	1.9	3338	9	US-09-789-919-45	Sequence 45, Appl
729	26	1.9	3408	9	US-09-789-919-20	Sequence 20, Appl
c 730	26	1.9	5647	13	US-10-311-455-1539	Sequence 1539, Ap
c 731	26	1.9	6165	10	US-09-880-107-3866	Sequence 3866, Ap
c 732	26	1.9	6352	13	US-10-311-455-877	Sequence 877, App
c 733	26	1.9	6352	15	US-10-172-086-23	Sequence 23, Appl
734	26	1.9	6553	11	US-09-764-872-952	Sequence 952, App
c 735	26	1.9	6668	13	US-10-311-455-1670	Sequence 1670, Ap
c 736	26	1.9	6686	13	US-10-311-455-434	Sequence 434, App
c 737	26	1.9	6854	10	US-09-764-877-3784	Sequence 3784, Ap
c 738	26	1.9	7921	13	US-10-311-455-1943	Sequence 1943, Ap
c 739	26	1.9	8912	8	US-08-424-550B-11	Sequence 11, Appl
c 740	26	1.9	9143	8	US-08-424-550B-390	Sequence 390, App
c 741	26	1.9	9143	8	US-08-424-550B-393	Sequence 393, App
c 742	26	1.9	9399	9	US-09-742-659-1	Sequence 1, Appli
c 743	26	1.9	10891	13	US-10-311-455-437	Sequence 437, App
c 744	26	1.9	16170	13	US-10-311-455-1241	Sequence 1241, Ap
c 745	26	1.9	20020	10	US-09-764-846-325	Sequence 325, App
746	26	1.9	20020	11	US-09-764-891-8223	Sequence 8223, Ap
c 747	26	1.9	20020	15	US-10-091-483-325	Sequence 325, App
c 748	26	1.9	21423	10	US-09-764-877-2835	Sequence 2835, Ap
749	26	1.9	32767	13	US-10-004-113-1	Sequence 1, Appli
750	26	1.9	44848	10	US-09-776-874A-42	Sequence 42, Appl
751	26	1.9	44848	10	US-09-988-113-42	Sequence 42, Appl
752	26	1.9	44848	13	US-10-341-582-42	Sequence 42, Appl
753	26	1.9	44848	13	US-10-384-451-42	Sequence 42, Appl
754	26	1.9	44848	13	US-10-384-450-42	Sequence 42, Appl
755	26	1.9	44848	13	US-10-371-218A-42	Sequence 42, Appl
756	26	1.9	46718	10	US-09-816-093-3	Sequence 3, Appli
757	26	1.9	46718	15	US-10-274-873-3	Sequence 3, Appli
c 758	26	1.9	48436	9	US-09-927-602-38	Sequence 38, Appl
c 759	26	1.9	113515	13	US-10-311-455-2148	Sequence 2148, Ap
760	26	1.9	152331	14	US-10-095-407-16	Sequence 16, Appl
761	26	1.9	167343	9	US-09-962-436-281	Sequence 281, App
762	26	1.9	167343	10	US-09-964-824A-273	Sequence 273, App
c 763	26	1.9	173808	14	US-10-003-806-10	Sequence 10, Appl
c 764	26	1.9	175590	11	US-09-911-077A-13	Sequence 13, Appl
765	26	1.9	176373	14	US-10-095-407-17	Sequence 17, Appl
c 766	26	1.9	180557	14	US-10-003-806-6	Sequence 6, Appli
c 767	26	1.9	180557	14	US-10-003-806-9	Sequence 9, Appli
768	26	1.9	3673778	13	US-10-312-841-2	Sequence 2, Appli
769	25	1.8	47	11	US-09-764-891-10177	Sequence 10177, A
c 770	25	1.8	58	13	US-09-898-860-42	Sequence 42, Appl
c 771	25	1.8	89	10	US-09-983-965-4255	Sequence 4255, Ap
c 772	25	1.8	101	9	US-09-770-696-896	Sequence 896, App
773	25	1.8	109	10	US-09-764-847-213	Sequence 213, App
774	25	1.8	109	15	US-10-092-154-213	Sequence 213, App
c 775	25	1.8	135	10	US-09-878-178-559	Sequence 559, App
c 776	25	1.8	135	14	US-10-046-935-559	Sequence 559, App
c 777	25	1.8	135	15	US-10-146-502-559	Sequence 559, App
c 778	25	1.8	150	15	US-10-066-543-2826	Sequence 2826, Ap
c 779	25	1.8	151	9	US-09-770-696-484	Sequence 484, App
c 780	25	1.8	153	10	US-09-933-797-793	Sequence 793, App
781	25	1.8	155	10	US-09-867-701-9298	Sequence 9298, Ap
c 782	25	1.8	158	9	US-09-770-696-429	Sequence 429, App
c 783	25	1.8	158	10	US-09-924-035A-493	Sequence 493, App
c 784	25	1.8	164	9	US-09-770-696-387	Sequence 387, App
785	25	1.8	168	10	US-09-867-701-9254	Sequence 9254, Ap
786	25	1.8	173	10	US-09-834-975-589	Sequence 589, App
787	25	1.8	173	10	US-09-867-701-9191	Sequence 9191, Ap
788	25	1.8	186	13	US-09-814-353-2459	Sequence 2459, Ap
789	25	1.8	186	13	US-09-814-353-8796	Sequence 8796, Ap
790	25	1.8	189	10	US-09-834-975-390	Sequence 390, App
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c 792	25	1.8	193	10	US-09-954-531-257	Sequence 257, App
793	25	1.8	197	10	US-09-867-701-9626	Sequence 9626, Ap
794	25	1.8	198	10	US-09-867-701-9198	Sequence 9198, Ap
795	25	1.8	198	15	US-10-113-234-3	Sequence 3, Appli
c 796	25	1.8	199	13	US-10-027-632-175908	Sequence 175908,
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799	25	1.8	210	10	US-09-867-701-9372	Sequence 9372, Ap
800	25	1.8	210	10	US-09-983-965-711	Sequence 711, App
c 801	25	1.8	211	13	US-10-027-632-144767	Sequence 144767,
c 802	25	1.8	211	14	US-10-027-632-144767	Sequence 144767,
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804	25	1.8	222	10	US-09-834-975-392	Sequence 392, App
c 805	25	1.8	230	13	US-09-814-353-15504	Sequence 15504, A
c 806	25	1.8	231	13	US-09-873-319-249	Sequence 249, App
c 807	25	1.8	231	13	US-09-960-706-417	Sequence 417, App
808	25	1.8	234	15	US-10-102-524-1382	Sequence 1382, Ap
c 809	25	1.8	236	13	US-09-814-353-4713	Sequence 4713, Ap
c 810	25	1.8	236	13	US-09-814-353-11011	Sequence 11011, A
c 811	25	1.8	255	13	US-09-930-213-584	Sequence 584, App
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813	25	1.8	263	14	US-10-027-632-267228	Sequence 267228,
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816	25	1.8	281	9	US-09-815-343-1303	Sequence 1303, Ap
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818	25	1.8	284	14	US-10-027-632-256018	Sequence 256018,

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c	821	25	1.8	292	14	US-10-040-739-1313	Sequence 1313, Ap
	822	25	1.8	296	10	US-09-867-701-9532	Sequence 9532, Ap
	823	25	1.8	297	10	US-09-867-701-6769	Sequence 6769, Ap
	824	25	1.8	297	10	US-09-867-701-9487	Sequence 9487, Ap
	825	25	1.8	297	10	US-09-867-701-10581	Sequence 10581, A
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c	827	25	1.8	306	13	US-09-814-353-5239	Sequence 5239, Ap
c	828	25	1.8	306	13	US-09-814-353-11526	Sequence 11526, A
	829	25	1.8	307	10	US-09-764-877-3509	Sequence 3509, Ap
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c	831	25	1.8	310	15	US-10-040-862-8537	Sequence 8537, Ap
	832	25	1.8	316	11	US-09-918-995-8182	Sequence 8182, Ap
	833	25	1.8	322	15	US-10-060-036-3330	Sequence 3330, Ap
	834	25	1.8	325	10	US-09-764-846-30	Sequence 30, Appl
	835	25	1.8	325	15	US-10-091-483-30	Sequence 30, Appl
	836	25	1.8	328	13	US-09-814-353-4803	Sequence 4803, Ap
	837	25	1.8	328	13	US-09-814-353-11100	Sequence 11100, A
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	839	25	1.8	332	11	US-09-918-995-11438	Sequence 11438, A
c	840	25	1.8	332	15	US-10-040-862-5438	Sequence 5438, Ap
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	842	25	1.8	334	11	US-09-918-995-15303	Sequence 15303, A
c	843	25	1.8	334	11	US-09-764-891-7914	Sequence 7914, Ap
c	844	25	1.8	335	15	US-10-060-036-1527	Sequence 1527, Ap
c	845	25	1.8	337	10	US-09-834-975-411	Sequence 411, App
c	846	25	1.8	338	10	US-09-878-178-1160	Sequence 1160, Ap
c	847	25	1.8	338	14	US-10-046-935-1160	Sequence 1160, Ap
c	848	25	1.8	338	15	US-10-146-502-1160	Sequence 1160, Ap
c	849	25	1.8	343	15	US-10-066-543-2452	Sequence 2452, Ap
c	850	25	1.8	345	13	US-09-814-353-18927	Sequence 18927, A
c	851	25	1.8	346	10	US-09-924-035A-547	Sequence 547, App
	852	25	1.8	351	10	US-09-983-965-3574	Sequence 3574, Ap
c	853	25	1.8	352	9	US-09-770-791-677	Sequence 677, App
c	854	25	1.8	361	10	US-09-960-352-4832	Sequence 4832, Ap
c	855	25	1.8	362	10	US-09-960-352-8132	Sequence 8132, Ap
	856	25	1.8	363	11	US-09-918-995-18123	Sequence 18123, A
c	857	25	1.8	364	13	US-09-814-353-17386	Sequence 17386, A
c	858	25	1.8	370	9	US-09-813-358-79	Sequence 79, Appl
c	859	25	1.8	370	10	US-09-867-701-10351	Sequence 10351, A
c	860	25	1.8	370	11	US-09-997-279-79	Sequence 79, Appl
c	861	25	1.8	373	15	US-10-060-036-1140	Sequence 1140, Ap
	862	25	1.8	375	11	US-09-918-995-2956	Sequence 2956, Ap
c	863	25	1.8	377	10	US-09-960-352-521	Sequence 521, App
c	864	25	1.8	378	15	US-10-066-543-1722	Sequence 1722, Ap
	865	25	1.8	379	10	US-09-960-352-7351	Sequence 7351, Ap
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c	868	25	1.8	381	13	US-10-027-632-284316	Sequence 284316,
c	869	25	1.8	381	13	US-10-027-632-284317	Sequence 284317,
c	870	25	1.8	381	13	US-10-027-632-284318	Sequence 284318,
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c	872	25	1.8	381	14	US-10-027-632-284316	Sequence 284316,
c	873	25	1.8	381	14	US-10-027-632-284317	Sequence 284317,
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	876	25	1.8	382	11	US-09-918-995-7567	Sequence 7567, Ap
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	879	25	1.8	384	13	US-09-814-353-5460	Sequence 5460, Ap
	880	25	1.8	384	13	US-09-814-353-11747	Sequence 11747, A
c	881	25	1.8	391	13	US-09-814-353-17395	Sequence 17395, A
c	882	25	1.8	392	10	US-09-960-352-2634	Sequence 2634, Ap
	883	25	1.8	394	9	US-09-817-318-16	Sequence 16, Appl
c	884	25	1.8	397	10	US-09-960-352-13784	Sequence 13784, A
	885	25	1.8	397	11	US-09-918-995-16211	Sequence 16211, A
c	886	25	1.8	398	10	US-09-960-352-12846	Sequence 12846, A
c	887	25	1.8	400	10	US-09-960-352-2891	Sequence 2891, Ap
c	888	25	1.8	401	9	US-09-795-668-1506	Sequence 1506, Ap
c	889	25	1.8	401	9	US-09-795-686-1506	Sequence 1506, Ap
c	890	25	1.8	401	10	US-09-946-807-1506	Sequence 1506, Ap
c	891	25	1.8	404	10	US-09-960-352-10751	Sequence 10751, A
c	892	25	1.8	405	9	US-09-795-668-1451	Sequence 1451, Ap
c	893	25	1.8	405	9	US-09-795-686-1451	Sequence 1451, Ap
c	894	25	1.8	405	10	US-09-946-807-1451	Sequence 1451, Ap
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c	898	25	1.8	410	15	US-10-198-846-13374	Sequence 13374, A
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	902	25	1.8	414	11	US-09-918-995-3592	Sequence 3592, Ap
	903	25	1.8	415	10	US-09-960-352-10021	Sequence 10021, A
	904	25	1.8	416	11	US-09-918-995-6498	Sequence 6498, Ap
	905	25	1.8	416	13	US-10-076-747-35	Sequence 35, Appl
	906	25	1.8	418	9	US-09-925-299-319	Sequence 319, App
	907	25	1.8	418	11	US-09-925-299-319	Sequence 319, App
	908	25	1.8	419	11	US-09-918-995-5669	Sequence 5669, Ap
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c	910	25	1.8	424	10	US-09-924-035A-800	Sequence 800, App
c	911	25	1.8	425	10	US-09-960-352-7925	Sequence 7925, Ap
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	915	25	1.8	436	13	US-09-814-353-17851	Sequence 17851, A
	916	25	1.8	439	11	US-09-918-995-5639	Sequence 5639, Ap
	917	25	1.8	441	13	US-10-027-632-280424	Sequence 280424,
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c	922	25	1.8	445	9	US-09-770-444-807	Sequence 807, App
	923	25	1.8	446	9	US-09-813-358-103	Sequence 103, App
	924	25	1.8	446	11	US-09-997-279-103	Sequence 103, App
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	927	25	1.8	446	13	US-10-027-632-284334	Sequence 284334,
	928	25	1.8	446	14	US-10-027-632-284332	Sequence 284332,
	929	25	1.8	446	14	US-10-027-632-284333	Sequence 284333,
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	932	25	1.8	452	11	US-09-918-995-5374	Sequence 5374, Ap
c	933	25	1.8	454	9	US-09-813-358-84	Sequence 84, Appl
c	934	25	1.8	454	11	US-09-997-279-84	Sequence 84, Appl
c	935	25	1.8	454	11	US-09-918-995-29548	Sequence 29548, A
	936	25	1.8	456	11	US-09-918-995-15545	Sequence 15545, A
	937	25	1.8	457	13	US-10-027-632-276428	Sequence 276428,
	938	25	1.8	457	14	US-10-027-632-276428	Sequence 276428,
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	940	25	1.8	458	15	US-10-198-846-13935	Sequence 13935, A
	941	25	1.8	461	15	US-10-074-475-38	Sequence 38, Appl
c	942	25	1.8	463	15	US-10-198-846-2523	Sequence 2523, Ap
	943	25	1.8	466	15	US-10-198-846-11483	Sequence 11483, A
	944	25	1.8	468	11	US-09-918-995-3981	Sequence 3981, Ap
	945	25	1.8	468	11	US-09-918-995-14744	Sequence 14744, A
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c	947	25	1.8	469	13	US-10-099-926-1001	Sequence 1001, Ap
c	948	25	1.8	469	14	US-10-033-528-1001	Sequence 1001, Ap
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	954	25	1.8	476	11	US-09-918-995-4738	Sequence 4738, Ap
	955	25	1.8	476	15	US-10-066-543-120	Sequence 120, App
c	956	25	1.8	477	15	US-10-198-846-516	Sequence 516, App
c	957	25	1.8	478	13	US-10-027-632-77537	Sequence 77537, A
c	958	25	1.8	478	14	US-10-027-632-77537	Sequence 77537, A
	959	25	1.8	478	15	US-10-102-806-172	Sequence 172, App
	960	25	1.8	480	10	US-09-878-574-4613	Sequence 4613, Ap
	961	25	1.8	481	13	US-10-027-632-192772	Sequence 192772,
	962	25	1.8	481	14	US-10-027-632-192772	Sequence 192772,
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	964	25	1.8	486	11	US-09-918-995-7387	Sequence 7387, Ap

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969	25	1.8	490	15	US-10-198-846-2580	Sequence 2580, Ap
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973	25	1.8	491	14	US-10-027-632-321065	Sequence 321065,
974	25	1.8	492	13	US-10-027-632-56690	Sequence 56690, A
975	25	1.8	492	13	US-10-027-632-56691	Sequence 56691, A
976	25	1.8	492	13	US-10-027-632-56692	Sequence 56692, A
977	25	1.8	492	13	US-10-027-632-297675	Sequence 297675,
978	25	1.8	492	13	US-10-027-632-297676	Sequence 297676,
979	25	1.8	492	13	US-10-027-632-297677	Sequence 297677,
980	25	1.8	492	14	US-10-027-632-56690	Sequence 56690, A
981	25	1.8	492	14	US-10-027-632-56691	Sequence 56691, A
982	25	1.8	492	14	US-10-027-632-56692	Sequence 56692, A
983	25	1.8	492	14	US-10-027-632-297675	Sequence 297675,
984	25	1.8	492	14	US-10-027-632-297676	Sequence 297676,
985	25	1.8	492	14	US-10-027-632-297677	Sequence 297677,
c 986	25	1.8	492	15	US-10-198-846-1562	Sequence 1562, Ap
c 987	25	1.8	493	10	US-09-924-035A-28	Sequence 28, Appl
988	25	1.8	495	13	US-10-027-632-81094	Sequence 81094, A
989	25	1.8	495	14	US-10-027-632-81094	Sequence 81094, A
990	25	1.8	498	13	US-09-814-353-15180	Sequence 15180, A
c 991	25	1.8	506	10	US-09-879-536-746	Sequence 746, App
992	25	1.8	510	10	US-09-867-701-6763	Sequence 6763, Ap
c 993	25	1.8	512	13	US-10-027-632-272884	Sequence 272884,
c 994	25	1.8	512	14	US-10-027-632-272884	Sequence 272884,
995	25	1.8	513	13	US-10-027-632-174786	Sequence 174786,
996	25	1.8	513	13	US-10-027-632-174787	Sequence 174787,
997	25	1.8	513	13	US-10-027-632-269959	Sequence 269959,
998	25	1.8	513	14	US-10-027-632-174786	Sequence 174786,
999	25	1.8	513	14	US-10-027-632-174787	Sequence 174787,
1000	25	1.8	513	14	US-10-027-632-269959	Sequence 269959,

ALIGNMENTS

RESULT 1
US-09-989-919-15
; Sequence 15, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prc
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1397
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-919-15

Query Match 100.0%; Score 1397; DB 10; Length 1397;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GGTGCTGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGCTGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTAC 60

Qy         61 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATC 120

Qy        121 CTACCACCACGGGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTACCACCACGGGAGCTGCCTCCTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTG 180

Qy        181 TGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGAGAGCCATGCCCAGTGTCGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTGA 240

Qy        241 GCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAGATAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCAGTGGGAGAAGCCCTTCCAAGGGAGATGGCAGGACCTCTCTGGAGGTTGATAGATAG 300

Qy        301 TGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGTGTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGATCCCCCATCGGAAGTCAGAGGGGGTGCTGAGGTGATGAGAGAGAGGTATACGTGTCT 360

Qy        361 TCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGCCCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCAAGGCAGTCAAATTAGGGAGAATGGTCTTGCCTCCAGAAAGAGAAACATCCAGCCCTG 420

Qy        421 TTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGGAGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTACCTCTCACCTCTGCCCCCCAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGGAGCC 480

Qy        481 AAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATCTGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGCTGACCTATCTGAG 540

Qy        541 GGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTGGAGGGAGTGACTT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTGGAGGGAGTGACTT 600

Qy        601 GCACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCAGACAAAGCTAACATCCCAGACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCACTGGCAGCACTGCATGTCACCTGGGAACCCCTGCAGACAAAGCTAACATCCCAGACA 660

Qy        661 GACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCAG 720

Qy        721 CCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCA 780

Qy        781 ACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCT 840

Qy        841 GGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGAATGTAGCTAAAGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGACGGTTCCGTGGGCAGCCCCATCACTGTGTTCAATAGTGTGAGAATGTAGCTAAAGC 900

Qy        901 CCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCGTGGGGACAATCCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCGTGGGGACAATCCA 960

Qy        961 TCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGGGGATGCTCCAGGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGGGGATGCTCCAGGA 1020

Qy       1021 TGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAGGGGACACTCCCAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAGGGGACACTCCCAG 1080

Qy       1081 GCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCAAGACTGGGGTCAG 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCTCAGCATGAGCCAAGACTGGGGTCAG 1140
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Qy       1141 GGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGGGGCCTTTCTGCCT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGGGGGTGGGGCCGGGGCCTTTCTGCCT 1200

Qy       1201 CATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGT 1260

Qy       1261 TTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAAT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TTGAATATCCAGAATCTTTTGTACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAAT 1320

Qy       1321 AAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACTCTTCCCTAAAAAAAAAAAA 1380

Qy       1381 AAAAAAAAAAGGCGGTC 1397
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Db       1381 AAAAAAAAAAGGCGGTC 1397
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RESULT 2
US-10-006-285-474
; Sequence 474, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
; APPLICANT: Mary Jane Cunningham
; APPLICANT: Matthew R. Kaser
; TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
; FILE REFERENCE: PA-0039 US
; CURRENT APPLICATION NUMBER: US/10/006,285
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PERL Program
; SEQ ID NO 474
; LENGTH: 1714
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165854A1 018653.18
US-10-006-285-474

Query Match 62.7%; Score 876; DB 13; Length 1714;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 926; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        442 CAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGGAGCCAAGTGGTCCCTGATCCCAACA 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CAGGTCGGCAGCTGGTCTTTTTCAAGACTGGATGGAGCCAAGTGGTCCCTGATCCCAACA 847

Qy        502 AGACCACATATGTGAAGGCCTCTGGCTGACCTATCTGAGGGCTCGGCTGACCAGCTGACT 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 AGACCACATATGTGAAGGCCTCTGGCTGACCTATCTGAGGGCTCGGCTGACCAGCTGACT 907

Qy        562 ATCCTCAGCAGCTGGGCTTGCCTGTGGAGGGAGTGACTTGCACTGGCAGCACTGCATGTC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 ATCCTCAGCAGCTGGGCTTGCCTGTGGAGGGAGTGACTTGCACTGGCAGCACTGCATGTC 967

Qy        622 ACCTGGGAACCCCTGCAGACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAA 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 ACCTGGGAACCCCTGCAGACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAA 1027

Qy        682 CGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGC 741
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Db       1028 CGTGCAATAATGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGC 1087

Qy        742 TCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAG 801
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Db       1088 TCCTAGTCCAGGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAG 1147

Qy        802 CTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCC 861
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Db       1148 CTCAGGCTAGTCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCC 1207

Qy        862 CCATCACTGTGTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 CCATCACTGTGTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACA 1267

Qy        922 TGCCACAGCAGGCGGTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCT 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 TGCCACAGCAGGCGGTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCT 1327

Qy        982 TAGGTCTGGACAGGAGACTTGGCGGGGGATGCTCCAGGATGTGGGTGATTCTGTACCTGG 1041
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Db       1328 TAGGTCTGGACAGGAGACTTGGCGGGAGATGCTCCAGGATGTGGGTGATTCTGTACCTGG 1387

Qy       1042 GGAGGCTATCTCTGACCTCCCGACAGGGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGC 1101
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Db       1388 GGAGGCTATCTCTGACCTCCCGACAGGGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGC 1447

Qy       1102 AGAGGTGCACACCTCAGCATGAGCCAAGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCC 1161
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Db       1448 AGAGGTGCACACCTCAGCATGAGCCAAGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCC 1507

Qy       1162 AGGACCTGGGGCGGGGGTGGGGCCGGGGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCC 1221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 AGGACCTGGGGCGGGGGTGGGGCCGGGGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCC 1567

Qy       1222 TCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTG 1281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 TCAAAGCAGCCAAAACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTG 1627

Qy       1282 TACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAA 1341
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Db       1628 TACTTCTTGTTGGTTAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAA 1687

Qy       1342 ATGATGTTTCACAGCAAACTCTTCCCT 1368
              ||||||||||||||||||||||||||
Db       1688 ATGATGTTTCACAGCAAACTCTTCCCT 1714
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RESULT 3
US-09-989-919-14
; Sequence 14, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-989-919-14

Query Match 31.6%; Score 442; DB 10; Length 470;
Best Local Similarity 100.0%; Pred. No. 6.5e-209;
Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        572 GCTGGGCTTGCCTGTGGAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTGGGAAC 631
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 GCTGGGCTTGCCTGTGGAGGGAGTGACTTGCACTGGCAGCACTGCATGTCACCTGGGAAC 66

Qy        632 CCCTGCAGACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAA 691
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Db        67 CCCTGCAGACAAAGCTAACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAA 126

Qy       692 TGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCA 751
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Db       127 TGCCAAATGTTAAAATGTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCA 186

Qy       752 GGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAG 811
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       187 GGAATCATGGGGGTATGACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAG 246

Qy       812 TCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGT 871
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Db       247 TCTCCCCACTGGGGGCTGTGCCCCTCCCTGGGACGGTTCCGTGGGCAGCCCCATCACTGT 306

Qy       872 GTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCACAGCA 931
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       307 GTTCAATAGTGTGAGAATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCACAGCA 366

Qy       932 GGCGGTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGA 991
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       367 GGCGGTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGA 426

Qy       992 CAGGAGACTTGGCGGGGGATGC 1013
            ||||||||||||||||||||||
Db       427 CAGGAGACTTGGCGGGGGATGC 448


RESULT 4
US-09-880-107-1138/c
; Sequence 1138, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1138
;   LENGTH: 427
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA451877
US-09-880-107-1138

  Query Match             23.0%;  Score 322;  DB 10;  Length 427;
  Best Local Similarity   99.5%;  Pred. No. 2.4e-149;
  Matches  422;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       936 GTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGG 995
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       427 GTGGGGGCTGCGTGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGG 368

Qy       996 AGACTTGGCGGGGGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTG 1055
            |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       367 AGACTTGGCGGGAGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTG 308

Qy      1056 ACCTCCCGACAGGGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCT 1115
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       307 ACCTCCCGACAGGGGACACTCCCAGGCCAGCCCAGGGGTCAGGGGCAGAGGTGCACACCT 248

Qy      1116 CAGCATGAGCCAAGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGG 1175
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       247 CAGCATGAGCCAAGACTGGGGTCAGGGAGCAGGTGTGGTTTGAGCCAGGACCTGGGGCGG 188

Qy      1176 GGGTGGGGCCGGGGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAA 1235
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       187 GGGTGGGACCGGGGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAA 128

Qy      1236 ACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGT 1295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       127 ACCAGGCTTTCCCCCTTCCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTTGGT 68

Qy      1296 TAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAG 1355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        67 TAAATTGTTTATTTTTGTAAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAG 8

Qy      1356 CAAA 1359
            ||||
Db         7 CAAA 4


RESULT 5
US-09-918-995-32213
; Sequence 32213, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32213
;   LENGTH: 493
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(493)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32213

  Query Match             6.9%;  Score 97;  DB 11;  Length 493;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-37;
  Matches   97;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         1 GGTGCTGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTAC 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       397 GGTGCTGCACCTGTACCGGAGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTAC 456

Qy        61 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAG 97
            |||||||||||||||||||||||||||||||||||||
Db       457 CGAGTACCAGTGTATCCCAGACAGCACCATCCCCCAG 493


RESULT 6
US-10-006-285-304
; Sequence 304, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
;  APPLICANT: Mary Jane Cunningham
;  APPLICANT:  Matthew R. Kaser
;  TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
;  FILE REFERENCE: PA-0039 US
;  CURRENT APPLICATION NUMBER: US/10/006,285
;  CURRENT FILING DATE:  2001-12-05
;  NUMBER OF SEQ ID NOS: 514
;  SOFTWARE: PERL Program
; SEQ ID NO 304
;   LENGTH: 1358
;   TYPE: DNA
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;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030165854A1 218659_Rn.1
US-10-006-285-304

  Query Match             2.6%;  Score 36;  DB 13;  Length 1358;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-07;
  Matches   36;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        203 GCCTTTGTGGTCACCAACCAGACCACCTGGACAGGT 238
              |||||||||||||||||||||||||||||||||||||
Db        461 GCCTTTGTGGTCACCAACCAGACCACCTGGACAGGT 496


RESULT 7
US-09-770-791-70/c
; Sequence 70, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
;  APPLICANT: Gorlach, Jorn
;  APPLICANT:  An, Yong-Qiang
;  APPLICANT:  Hamilton, Carol M.
;  APPLICANT:  Price, Jennifer L.
;  APPLICANT:  Raines, Tracy M.
;  APPLICANT:  Yu, Yang
;  APPLICANT:  Rameaka, Joshua G.
;  APPLICANT:  Page, Amy
;  APPLICANT:  Matthew, Abraham V.
;  APPLICANT:  Ledford, Brooke L.
;  APPLICANT:  Woessner, Jeffrey P.
;  APPLICANT:  Haas, William David
;  APPLICANT:  Garcia, Carlos A.
;  APPLICANT:  Kricker, Maja
;  APPLICANT:  Slader, Ted
;  APPLICANT:  Davis, Keith R.
;  APPLICANT:  Allen, Keith
;  APPLICANT:  Hoffman, Neil
;  APPLICANT:  Hurban, Patrick
;  TITLE OF INVENTION: Expressed Sequences of Arabidopsis
;  TITLE OF INVENTION:  thaliana
;  FILE REFERENCE: 2029 (PARA-018PRV)
;  CURRENT APPLICATION NUMBER: US/09/770,791
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: 60/178,480
;  PRIOR FILING DATE: 2000-01-27
;  NUMBER OF SEQ ID NOS: 999
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
;   LENGTH: 386
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-770-791-70

  Query Match             2.1%;  Score 30;  DB 9;  Length 386;
  Best Local Similarity   100.0%;  Pred. No. 0.00022;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              ||||||||||||||||||||||||||||||
Db         31 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 8
US-09-867-701-3641/c
; Sequence 3641, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;  APPLICANT: Aglate, Paul A.
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE:  2001-05-29
;  NUMBER OF SEQ ID NOS: 10912
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3641
;   LENGTH: 421
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-867-701-3641

  Query Match             2.1%;  Score 30;  DB 10;  Length 421;
  Best Local Similarity   100.0%;  Pred. No. 0.00022;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              ||||||||||||||||||||||||||||||
Db         30 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 9
US-09-770-445-884/c
; Sequence 884, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
;  APPLICANT:  Gorlach, Jorn
;  APPLICANT:  An, Yong-Qiang
;  APPLICANT:  Hamilton, Carol M.
;  APPLICANT:  Price, Jennifer L.
;  APPLICANT:  Raines, Tracy M.
;  APPLICANT:  Yu, Yang
;  APPLICANT:  Rameaka, Joshua G.
;  APPLICANT:  Page, Amy
;  APPLICANT:  Matthew, Abraham V.
;  APPLICANT:  Ledford, Brooke L.
;  APPLICANT:  Woessner, Jeffrey P.
;  APPLICANT:  Haas, William David
;  APPLICANT:  Garcia, Carlos A.
;  APPLICANT:  Kricker, Maja
;  APPLICANT:  Slader, Ted
;  APPLICANT:  Davis, Keith R.
;  APPLICANT:  Allen, Keith
;  APPLICANT:  Hoffman, Neil
;  APPLICANT:  Hurban, Patrick
;  TITLE OF INVENTION:  Expressed Sequences of Arabidopsis
;  TITLE OF INVENTION:  thaliana
;  FILE REFERENCE:  2023US (PARA-012PRV)
;  CURRENT APPLICATION NUMBER: US/09/770,445
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER:  US 60/178,472
;  PRIOR FILING DATE:  2000-01-27
;  NUMBER OF SEQ ID NOS:  999
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 884
;   LENGTH: 777
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-770-445-884

  Query Match             2.1%;  Score 30;  DB 9;  Length 777;
  Best Local Similarity   100.0%;  Pred. No. 0.00021;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
              ||||||||||||||||||||||||||||||
Db         45 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 10
US-10-199-672-569
; Sequence 569, Application US/10199672
; Publication No. US20030148442A1
; GENERAL INFORMATION:
```

; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/199,672
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 569
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-672-569

Query Match 2.1%; Score 30; DB 13; Length 2457;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||||||
Db 2423 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 2452

RESULT 11
US-10-187-749-569
; Sequence 569, Application US/10187749
; Publication No. US20030153036A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/187,749
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 569
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-187-749-569

Query Match 2.1%; Score 30; DB 13; Length 2457;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||||||
Db 2423 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 2452

RESULT 12
US-10-194-457-569
; Sequence 569, Application US/10194457
; Publication No. US20030153037A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 569
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-194-457-569

Query Match 2.1%; Score 30; DB 13; Length 2457;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||||||
Db 2423 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 2452

RESULT 13
US-10-184-642-569
; Sequence 569, Application US/10184642
; Publication No. US20030157635A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C194
; CURRENT APPLICATION NUMBER: US/10/184,642
; CURRENT FILING DATE: 2002-06-27
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 569
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-642-569

Query Match 2.1%; Score 30; DB 13; Length 2457;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||||||
Db 2423 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 2452

RESULT 14
US-10-196-747-569
; Sequence 569, Application US/10196747
; Publication No. US20030162250A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C346
; CURRENT APPLICATION NUMBER: US/10/196,747
; CURRENT FILING DATE: 2002-07-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 569
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-747-569

Query Match 2.1%; Score 30; DB 13; Length 2457;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||||||
Db 2423 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 2452

RESULT 15
US-10-173-689-569
; Sequence 569, Application US/10173689
; Publication No. US20030166104A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C10
; CURRENT APPLICATION NUMBER: US/10/173,689
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 569
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-173-689-569

Query Match 2.1%; Score 30; DB 13; Length 2457;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1361 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 1390
||||||||||||||||||||||||||||||
Db 2423 TCTTCCCTAAAAAAAAAAAAAAAAAAAAAA 2452

Search completed: December 13, 2003, 21:19:53
Job time : 385 secs